

```

? APPLICANT: Roy, Margaret Ann
? APPLICANT: Stewart, Timothy A.
? APPLICANT: Thomas, Daniel
? APPLICANT: Warrabee, Gerald K.
? APPLICANT: Williams, P. Mickey
? APPLICANT: Wood, William L.
? APPLICANT: Zhang, Zemin
? TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
? FILE REFERENCE: P27401048
? CURRENT APPLICATION NUMBER: US 09/043,177
? CURRENT FILING DATE: 2001-11-16
? PRIOR APPLICATION REMOVED: No Title Wrapper: 1 Title
? NUMBER OF SEQ ID NOS: 542
? SEQ ID NO 219
? LENGTH: 642
? TYPE: PRT
? ORGANISM: Homo sapiens
US-09-991-150-219

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Query Match 12.6% Score 146 ID 51 Length 642
Post Local Similarity 40.0% Pred. No. 6.5e-06
Matches 38; Conservative 13; Mismatches 36; Indels 8; Gaps 4;

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QY 105 HPEVHLPR-TDETCNPNVWGG---KEQNSIVYSKRIKGVAPRGHGKRIQGLISVNG 160
I : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
I : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
ID 408 HPEVNLTKRQPSSTQVAGASHPEWLPVIVSVESGVSISQPRIRKIDILLNVG 467
I : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
I : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 161 VSEVHHHFAVELLFAKISVLE---VVEVLR 191
I : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
ID 468 VELFVSKSAVALIKRISIVIKALEVEVYHQ 502
I : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

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RESULT 8
US-10-121-062-166

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```

? Sequence 166, Application US/10121062
? GENERAL INFORMATION:
? APPLICANT: Baker, Kevin P.
? APPLICANT: Gaudin,
? APPLICANT: Insnoyers, Luc
? APPLICANT: Reddard, Audrey
? APPLICANT: Gadowski, Paul J.
? APPLICANT: Gurney, Austin L.
? APPLICANT: Pan, James
? APPLICANT: Smith, Victoria
? APPLICANT: Watanabe, Colin K.
? APPLICANT: Wood, William L.
? APPLICANT: Zhang, Zemin
? TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
? FILE REFERENCE: P34308101
? CURRENT APPLICATION NUMBER: US 09/022,366
? CURRENT FILING DATE: 2002-04-12
? PRIOR APPLICATION REMOVED: See Title Wrapper of Paim
? NUMBER OF SEQ ID NOS: 612
? SEQ ID NO 166
? LENGTH: 642
? TYPE: PRT
? ORGANISM: Homo Sapien
US-10-121-062-166

```

```

Query Match 12.6% Score 146 ID 51 Length 642
Post Local Similarity 40.0% Pred. No. 6.5e-06
Matches 38; Conservative 13; Mismatches 36; Indels 8; Gaps 4;

```

```

QY 105 HPEVHLPR-TDETCNPNVWGG---KEQNSIVYSKRIKGVAPRGHGKRIQGLISVNG 160
I : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
I : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
ID 408 HPEVNLTKRQPSSTQVAGASHPEWLPVIVSVESGVSISQPRIRKIDILLNVG 467
I : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
I : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 161 VSEVHHHFAVELLFAKISVLE---VVEVLR 191
I : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
I : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

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ID 468 VELFVSKSAVALIKRISIVIKALEVEVYHQ 502

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RESULT 9

```

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US-10-106-698-5902
? Sequence 5902, Application US/10106698
? GENERAL INFORMATION:
? APPLICANT: Rubin et al.
? TITLE OF INVENTION: Colon and Colon Cancer Associated Polymorphisms and Polypep
? FILE REFERENCE: P600591
? CURRENT APPLICATION NUMBER: US 09/106,698
? CURRENT FILING DATE: 2002-03-27
? PRIOR APPLICATION REMOVED: No Title Wrapper: 1 Title
? PRIOR FILING DATE: 2000-09-28
? PRIOR APPLICATION NUMBER: US 60/157,137
? PRIOR FILING DATE: 1999-09-29
? PRIOR APPLICATION NUMBER: US 60/164,280
? PRIOR FILING DATE: 1999-11-03
? NUMBER OF SEQ ID NOS: 8564
? SOFTWARE: PatentIn Ver. 3.0
? SEQ ID NO 5902
? LENGTH: 227
? TYPE: PRT
? ORGANISM: Homo sapiens
? FEATURE:
? MAP: 333, 533, FEATURE
? LOCATION: (29)
? OTHER INFORMATION: X04 equals any of the naturally occurring L-amino acids
US-10-106-698-5902

```

```

Query Match 12.2% Score 142 ID 51 Length 227
Post Local Similarity 38.9% Pred. No. 5.9e-06
Matches 37; Conservative 11; Mismatches 39; Indels 8; Gaps 4;

```

```

QY 105 HPEVHLPR-TDETCNPNVWGG---PYSSEIPEQVAPRGHGKRIQGLISVNG 160
I : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
I : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
ID 408 HPEVNLTKRQPSSTQVAGASHPEWLPVIVSVESGVSISQPRIRKIDILLNVG 467
I : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
I : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 161 VSEVHHHFAVELLFAKISVLE---VVEVLR 191
I : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
ID 468 VELFVSKSAVALIKRISIVIKALEVEVYHQ 502
I : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

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RESULT 10

```

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US-60-365-264-266
? Sequence 266, Application US/60365264
? GENERAL INFORMATION:
? APPLICANT: Tang, Y. Tom
? APPLICANT: Wang, Jian-Fai
? APPLICANT: Wang, Zhiwei
? APPLICANT: Wang, Jian-Rui
? APPLICANT: Zhang, Jie
? APPLICANT: Ren, Feiyun
? APPLICANT: Zhou, Ping
? APPLICANT: Ma, Yanguo
? APPLICANT: Ghosh, Malabika
? APPLICANT: Xue, Aibang J.
? APPLICANT: Asundi, Vinod
? APPLICANT: Zhao, Qing A.
? APPLICANT: Wang, Dantui
? APPLICANT: Goodrich, Kyle W.
? APPLICANT: Chen, Kai-Tong
? APPLICANT: Weinman, Tom
? APPLICANT: Wood, Gerald
? TITLE OF INVENTION: Novel Nucleic Acids and
? FILE REFERENCE: 816
? CURRENT APPLICATION NUMBER: US 60/266,264
? CURRENT FILING DATE: 2002-03-14
? NUMBER OF SEQ ID NOS: 728
? SOFTWARE: PatentIn Version 3.0
? SEQ ID NO 266

```



## RESULT 2

US-09-909-069A-2

Sequence 2, Application US/09931969A

GENERAL INFORMATION:

APPLICANT: NICOLETTE, Charles A.

TITLE OF INVENTION: THERAPEUTIC COMPOUNDS FOR OVARIAN CANCER

FILE REFERENCE: 67/2104-00

CURRENT APPLICATION NUMBER: US/09/931-969A

CURRENT FILING DATE: 2002-04-08

PRIOR APPLICATION NUMBER: 60/225,213

PRIOR FILING DATE: 2000-08-17

NUMBER OF SEQ. ID NOS: 12

SOFTWARE: FASTSEQ for Windows Version 4.0

SEQ. ID NO. 2

LENGTH: 1266

TYPE: PRT

ORGANISM: Homo sapiens

US-09-909-069A-2

Query Match

Post Local Similarity 36.08; Score 167; DB 5; Length 1266

Matches 41; Conservative 25; Mismatches 32; Indels 16; Gaps 4

US-09-909-069A-2

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US-09-909-069A-2



```

US-09-270-767-48563
: Sequence 48563, Application US-09-270-767
: GENERAL INFORMATION:
: APPLICANT: Bomburger et al
: TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
: FILE REFERENCE: File Reference: 7326-094
: CURRENT APPLICATION NUMBER: US-09-270-767
: NUMBER OF SEQ ID NOS: 62517
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 48563
: LENGTH: 204
: TYPE: PRT
: ORGANISM: Drosophila melanogaster
US-09-270-767-48563

```

```

Query Match          64.4%; Score 754; DB 16; Length 204
Best Local Similarity 77.9%; Pred. No. 1,5e-61;
Matches 148; Conservative 20; Mismatches 22; Indels 0; Gaps 0;

```

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QY 21 GPTTIDGVAAATFETLPTVYSSPEVYVHPTGSEFVYNSLEPLALPEVYQYMHETLVNS 80
DB 15 EPLTSLKGVKSTLELLENLQASDFPLELALQVLSDFMTSVREYEHVETVDIOG 74
QY 81 GPEFPAATATKATVAATAFAASESHSPVVEIPKTDLSGFNMGCCKEONSPYISRTIPG 140
DB 75 SHDKASATATKATVAATAFAASEGHAPRVVELPKTELDLSGFNMGCCKEONSPYISRTIPG 134
QY 141 GVAERHGLTKRGDLSVNVSVSGGHHRAVETLKAATSVKLVVYVTEVLESEAPF 200
DB 135 GVAERHGLTKRGDLSVNVSVSGGHHRAVETLKAATSVKLVVYVTEVLESEAPF 194
QY 201 FKLPATPPQ 210
DB 195 DKGNTRKKQ 204

```

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RESULT 15
US-09-270-8498-191322
: Sequence 191322, Application US-09-270-8498
: GENERAL INFORMATION:
: APPLICANT: Swimmer et al.
: TITLE OF INVENTION: Insect genome survey devices
: FILE REFERENCE:
: CURRENT APPLICATION NUMBER: US-09-270-8498
: CURRENT FILING DATE: 1999-03-17
: NUMBER OF SEQ ID NOS: 195450
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 191322
: LENGTH: 204
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-270-8498-191322

```

```

Query Match          64.4%; Score 754; DB 16; Length 204
Best Local Similarity 77.9%; Pred. No. 1,5e-61;
Matches 148; Conservative 20; Mismatches 22; Indels 0; Gaps 0;

```

```

QY 21 GPTTIDGVAAATFETLPTVYSSPEVYVHPTGSEFVYNSLEPLALPEVYQYMHETLVNS 80
DB 15 EPLTSLKGVKSTLELLENLQASDFPLELALQVLSDFMTSVREYEHVETVDIOG 74
QY 81 GPEFPAATATKATVAATAFAASESHSPVVEIPKTDLSGFNMGCCKEONSPYISRTIPG 140
DB 75 SHDKASATATKATVAATAFAASEGHAPRVVELPKTELDLSGFNMGCCKEONSPYISRTIPG 134
QY 141 GVAERHGLTKRGDLSVNVSVSGGHHRAVETLKAATSVKLVVYVTEVLESEAPF 200
DB 135 GVAERHGLTKRGDLSVNVSVSGGHHRAVETLKAATSVKLVVYVTEVLESEAPF 194

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QY 201 FKLPATPPQ 210
DB 195 DKGNTRKKQ 204

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Search completed: May 7, 2002, 12:43:57
Job time: 211 sec

```



NUMBER OF SEQ ID NOS: 745  
 SOFTWARE: FASTSEQ for Windows Version 4.0  
 SEQ ID NO 369  
 LENGTH: 406  
 TYPE: PRT  
 ORGANISM: HUMAN  
 US-60-229-518-369

Query Match 67.98; Score 754; DB 24; Length 406  
 Best Local Similarity 82.18; Pred. No. 1.4e-61;  
 Matches 151; Conservative 21; Mismatches 12; Indels 0; Gaps 0;

QY 28 QVAFATPTPTTSPCVFVHPTGSLFKVCEFTTATETVTCYMETTVRGTCTTAP 87  
 DB 202 DVPATATITPTTSSGVTFVTALELVLESTFCAVAVETVIVHVLVQSSLVKAD 291  
 QY 88 ATAKATVAAPVAAAPASHSHPRVVPVPTTTEGLQFVNMCKEONSPVYISPIIPGVAEKRG 147  
 DB 282 ATAKATVAAPVAAASHSHPRVVEIPKTEFTGFMIMCKEONSPVYISPIIPGVAMPK 341  
 QY 148 GLKGGGGLISVNVSVSGSEHHEKAVELLKAAKDSVKLVVVTTPVKVLPFMAPPEKPTAP 207  
 DB 342 GLKPGGGLISVNVSVSGSEHHEKAVELLKAAKDSVKLVVVTTPVLEMESEPEKMSAR 401

QY 208 KRQD 211  
 DB 402 KRQD 405

RESULT 8  
 US-60-167-245-601  
 Sequence 601 Affiliation US/60167245  
 GENERAL INFORMATION:  
 APPLICANT: Li, Peter, W.D.  
 TITLE OF INVENTION: ISOLATED ION CHANNEL PROTEINS, NUCLEIC  
 TITLE OF INVENTION: ACID MOLECULES ENCODING ION CHANNEL PROTEINS AND USES  
 FILE REFERENCE: C1000151  
 CURRENT APPLICATION NUMBER: US/60167,245  
 CURRENT FILING DATE: 1999-11-24  
 NUMBER OF SEQ ID NOS: 789  
 SOFTWARE: FASTSEQ for Windows Version 4.0  
 SEQ ID NO 601  
 LENGTH: 195  
 TYPE: PRT  
 ORGANISM: Drosophila  
 US-60-167-245-601

Query Match 64.48; Score 754; DB 24; Length 195  
 Best Local Similarity 77.98; Pred. No. 1.4e-61;  
 Matches 148; Conservative 20; Mismatches 22; Indels 0; Gaps 0;

QY 21 QPTTDEPVAAATLLEELGSCGFVHKLQSLFKVCEFTTATETVTCYMETTVRGTCTTAP 90  
 DB 6 EPITLSKVKSTLEELKELKASGFPPTKLAALQVINSDFMISVEVYHVEVTVLQ 65  
 QY 81 QPFRATATATATVAAAPASHSHPRVVPVPTTTEGLQFVNMCKEONSPVYISPIIPGVAEKRG 140  
 DB 66 SHDVASATATATVAAAPASHSHPRVVEIPKTEFTGFMIMCKEONSPVYISPIIPGVAMPK 125  
 QY 141 QVAFPHQVTPVYGLISVNVSVSGSEHHEKAVELLKAAKDSVKLVVVTTPVKVLPFMAPPEKPTAP 200  
 DB 126 QVAFPHQVTPVYGLISVNVSVSGSEHHEKAVELLKAAKDSVKLVVVTTPVKVLPFMAPPEKPTAP 185  
 QY 281 EKLRTAKRQ 210  
 DB 186 DKQRTAKRQ 195

RESULT 9  
 US-60-173-463-14024

Sequence 14024 Affiliation US/60173464  
 GENERAL INFORMATION:  
 APPLICANT: Li, Peter W.D.  
 TITLE OF INVENTION: ISOLATED G-PROTEIN COUPLED RECEPTORS,  
 TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING GPCR PROTEINS AND USES  
 FILE REFERENCE: C1000173  
 CURRENT APPLICATION NUMBER: US/60173,464  
 CURRENT FILING DATE: 1999-12-29  
 NUMBER OF SEQ ID NOS: 30269  
 SOFTWARE: FASTSEQ for Windows Version 4.0  
 SEQ ID NO 14024  
 LENGTH: 195  
 TYPE: PRT  
 ORGANISM: Drosophila  
 US-60-173-463-14024

Query Match 64.48; Score 754; DB 24; Length 195  
 Best Local Similarity 77.98; Pred. No. 1.4e-61;  
 Matches 148; Conservative 20; Mismatches 22; Indels 0; Gaps 0;

QY 21 QPTTDEPVAAATLLEELGSCGFVHKLQSLFKVCEFTTATETVTCYMETTVRGTCTTAP 80  
 DB 6 EPITLSKVKSTLEELKELKASGFPPTKLAALQVINSDFMISVEVYHVEVTVLQ 65  
 QY 81 QPFRATATATATVAAAPASHSHPRVVPVPTTTEGLQFVNMCKEONSPVYISPIIPGVAEKRG 140  
 DB 66 SHDVASATATATVAAAPASHSHPRVVEIPKTEFTGFMIMCKEONSPVYISPIIPGVAMPK 125  
 QY 141 QVAFPHQVTPVYGLISVNVSVSGSEHHEKAVELLKAAKDSVKLVVVTTPVKVLPFMAPPEKPTAP 200  
 DB 126 QVAFPHQVTPVYGLISVNVSVSGSEHHEKAVELLKAAKDSVKLVVVTTPVKVLPFMAPPEKPTAP 185  
 QY 202 EKLRTAKRQ 210  
 DB 195 DKQRTAKRQ 195

RESULT 10  
 US-60-191-637-17123  
 Sequence 17123 Affiliation US/60191637  
 GENERAL INFORMATION:  
 APPLICANT: Venter, J. Craig  
 TITLE OF INVENTION: NUCLEIC ACID DETECTOR KITS COMPRISING  
 TITLE OF INVENTION: GENE SEQUENCES EXPRESSED FROM THE DROSOPHILA CHINER, AND  
 TITLE OF INVENTION: USES THEREOF  
 FILE REFERENCE: C1000392  
 CURRENT APPLICATION NUMBER: US/60191,637  
 CURRENT FILING DATE: 2000-03-23  
 NUMBER OF SEQ ID NOS: 42660  
 SOFTWARE: FASTSEQ for Windows Version 4.0  
 SEQ ID NO 17123  
 LENGTH: 195  
 TYPE: PRT  
 ORGANISM: DROSOPHILA  
 US-60-191-637-17123

Query Match 64.48; Score 754; DB 24; Length 195  
 Best Local Similarity 77.98; Pred. No. 1.4e-61;  
 Matches 148; Conservative 20; Mismatches 22; Indels 0; Gaps 0;

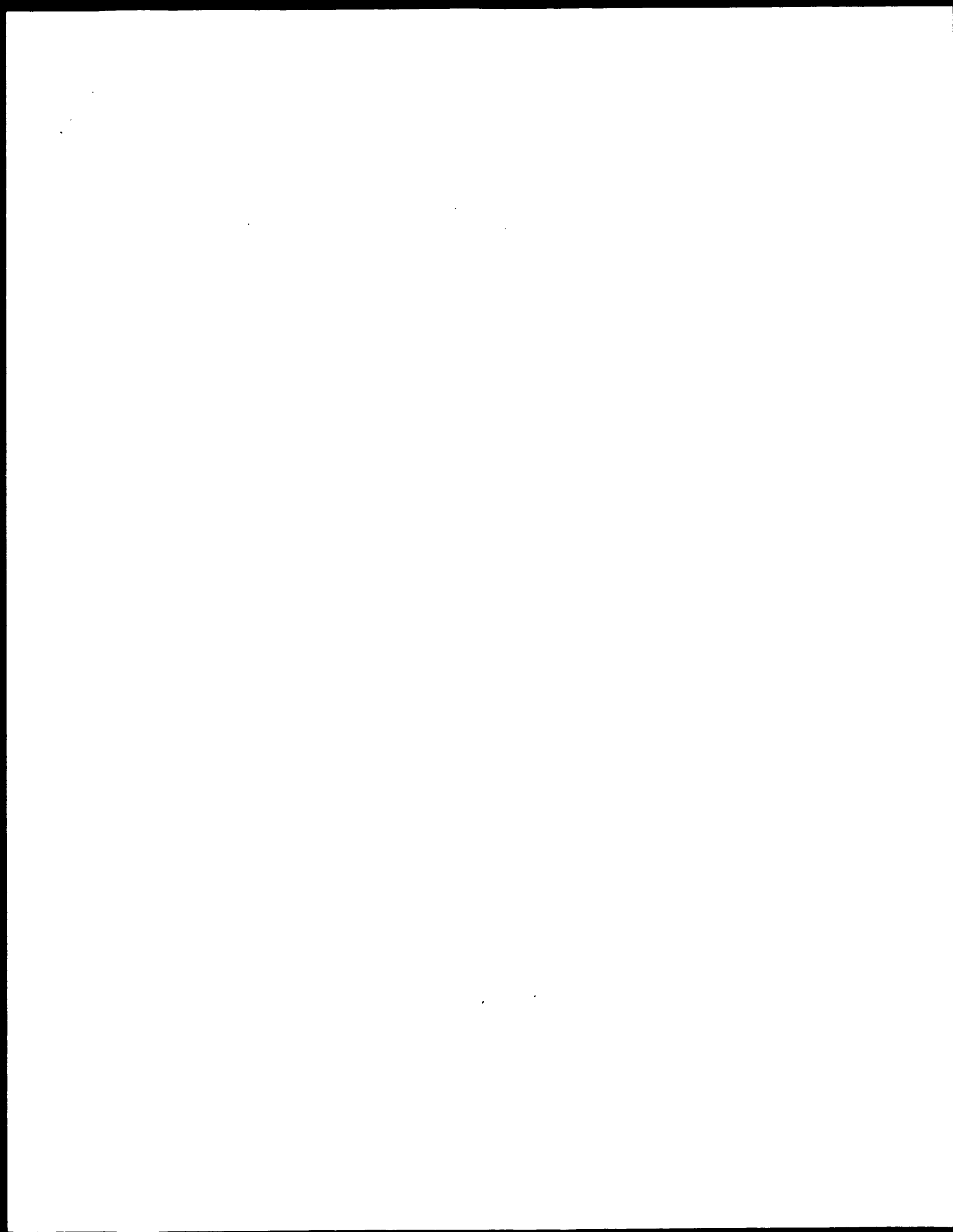
QY 21 QPTTDEPVAAATLLEELGSCGFVHKLQSLFKVCEFTTATETVTCYMETTVRGTCTTAP 80  
 DB 6 EPITLSKVKSTLEELKELKASGFPPTKLAALQVINSDFMISVEVYHVEVTVLQ 65  
 QY 81 QPFRATATATATVAAAPASHSHPRVVPVPTTTEGLQFVNMCKEONSPVYISPIIPGVAEKRG 140  
 DB 66 SHDVASATATATVAAAPASHSHPRVVEIPKTEFTGFMIMCKEONSPVYISPIIPGVAMPK 125  
 QY 141 QVAFPHQVTPVYGLISVNVSVSGSEHHEKAVELLKAAKDSVKLVVVTTPVKVLPFMAPPEKPTAP 200  
 DB 126 QVAFPHQVTPVYGLISVNVSVSGSEHHEKAVELLKAAKDSVKLVVVTTPVKVLPFMAPPEKPTAP 185













(RECD ) UNIV CALIFORNIA.

XX Brodt DS, Brennan JE, Chao DS.

XX WPL: 1997-470555/43.

XX N-PSDM; AAT93775.

XX Diagnostic muscular dystrophy by detecting absence or decrease of  
P1 neuronal nitric oxide synthase (nNOS) in skeletal muscle sarcolemma  
P1 - using new nNOS binding post-synaptic density proteins, PSD-93 and  
P1 PSD-95; also used for the diagnosis, prophylaxis and treatment of  
P1 stroke and other neurodegenerative diseases

XX claim 16; Page 74-76; 124pp; English.

XX This sequence is a partial sequence of post synaptic density / protein-93  
CC (PSD-93). PSD-93 can be used in the method of the invention for  
CC diagnostic muscular dystrophy (MD) in a mammal by detecting absence or a  
CC decrease of neuronal nitric oxide synthase (NOS) in a skeletal muscle  
CC sample. Put pools with presence or absence of PSD-93 and nNOS in  
CC skeletal muscle. In addition to lack of functional dystrophin, nNOS is  
CC normally targeted to the sarcolemma by associating to dystrophin (via the  
CC N-terminal PDZ domain (66 aa motif bearing homology to a heptapeptide  
CC family of signaling enzymes localized at cell-cell junctions) of nNOS,  
CC interacting specifically with the PDZ domain of the alpha 1 syntrophin  
CC component). The binding proteins PSD-93 and -95 also have a PDZ domain  
CC and interact with nNOS mediating binding of nNOS to the NMDA receptor  
CC located at synapses. The PSD proteins are involved in the development and  
CC progression of stroke and some neurodegenerative diseases (e.g.  
CC Huntington's and Alzheimer's diseases and amyotrophic lateral sclerosis).  
CC so inhibiting them (or their binding) can be used to treat one such  
CC diseases (associated with overactivation of NMDA receptors) or excessive  
CC levels of nNOS. This method allows early diagnosis of MD. MD can now be  
CC treated by gene therapy, using only the treatment of dystrophin involved  
CC in formation of the nNOS/sarcolemma/dystrophin complex, rather than the  
CC complete dystrophin gene which is too large to manipulate.

XX Sequence 862 AA:

Query Match 16.98; Score 147.5; DB 18; Length 832;

Best local Similarity 44.88; Pred. No. 36; 11;

Matches 49; Conservative 26; Mismatches 53; Indels 15; Gaps 3;

QY 88 ATAAATVAAATASGSHHPVETPKETEDGQNMVDEKQKQVYLSKINQVAMKQ 147

DB 414 ATGHSVLPFAISLPKPKVTHKSTLHITQFQEDGQVHSTLLAQGLDQ 472

QY 119 QPPTGTLVNVVGVCTHPPFAVPIPAAGVGVVNVVITKVLGAGATK 204

DB 473 elqfqtqkllsqvdlfpqshoqlp lkaqfvtllafpdyatckkhlrlqm 531

QY 205 -----TAREQQQGLTQ 217

DB 512 mlaamssqsgsltrkrslyvt 554

RESULT 13

AA022148

XX AAB22138 standard; pep1 id: 767 AA.

XX AAB22138;

XX 21-FEB-2001 (first entry)

XX Human post-synaptic density protein 95 PSD95.

XX Human post-synaptic density protein 95; PSD-95; PDZ domain; GluR1 loop;

XX Human post-synaptic density protein 95; PSD-95; PDZ domain; GluR1 loop;

XX Human post-synaptic density protein 95; PSD-95; PDZ domain; GluR1 loop;

XX Human post-synaptic density protein 95; PSD-95; PDZ domain; GluR1 loop;

XX Human post-synaptic density protein 95; PSD-95; PDZ domain; GluR1 loop;

XX Human post-synaptic density protein 95; PSD-95; PDZ domain; GluR1 loop;

XX Human post-synaptic density protein 95; PSD-95; PDZ domain; GluR1 loop;

XX Human post-synaptic density protein 95; PSD-95; PDZ domain; GluR1 loop;

XX Human post-synaptic density protein 95; PSD-95; PDZ domain; GluR1 loop;

XX Human post-synaptic density protein 95; PSD-95; PDZ domain; GluR1 loop;

XX Human post-synaptic density protein 95; PSD-95; PDZ domain; GluR1 loop;

XX 17-AUG-2000.

XX 09-FEB-2000; 2000W0-GH00374.

XX 09-FEB-1999; 99GB-0002696.

XX (MED1-) MEDICAL RES COUNCIL.

XX Spillanti MG, Goederl M, Hasegawa M, Huse-Schroter V, Thomas G.

XX Cohen P, Genda A;

XX WPL: 2000-55826/51.

XX Novel methods for identifying compounds useful for treating muscular

XX dystrophy comprising identifying modulators of protein kinase and PDZ

XX domain binding -

XX Disclosure; Fig 11, 12pp; English.

XX The present sequence is the protein sequence of the human post-synaptic  
CC density protein 95 (PSD-95). It is described with reference to the  
CC methods of the invention, which involve the identification of compounds  
CC which are able to modulate the interaction between PDZ domains (also  
CC known as PDZ or GluR domains) and protein kinases. The invention also  
CC comprises peptide fragments derived from stress-activated protein kinases  
CC which are involved in protein phosphorylation. The compounds and peptides  
CC can be used in the treatment of muscular diseases, for example muscular  
CC dystrophy, or in cases where modulation of phosphorylation of proteins  
CC with PDZ domains is modulation of signaling via activity receptors or  
CC voltage gated channels is necessary, or in instances where the  
CC localisation of SAPK3 at the neuromuscular junction or sarcolemma needs  
CC to be disrupted.

XX Sequence 767 AA:

Query Match 16.68; Score 194.5; DB 21; Length 767;

Best local Similarity 41.48; Pred. No. 150-10;

Matches 41; Conservative 19; Mismatches 38; Indels 1; Gaps 1;

QY 116 EAVVETLFTEDGSEFNVAGKQKQVYLSKINQVAMKQVLSVAVSNG 164

DB 354 prlvltqstqqltdvqv-odqgllslslldqpadlsq-lrkddllsqvndln 412

QY 156 EHNKAVETLPAKDSVGLVPTPVVLEHMAPEKIP 294

DB 413 asheqadldlkralqfvtllafpdyatckkhlrlqm 451

RESULT 14

AA024025

XX AAY24025 standard; Protein; 1881 AA.

XX AAY24025;

XX 29-SEP-1999 (first entry)

XX Amino acid sequence of the human MMS1 protein.

XX Human MMS1 protein; MMS1 interacting protein; tumour suppressor;

XX MMS1 pathway; Immunogen; cancer; cell neoplastic growth.

XX Homo sapiens.

XX W09936566-A1.

XX 22-JUL-1999.

XX 19-JAN-1999; 99W0-0500945.

XX 20-JAN-1998; 9808-0071861.

AAV30137  
 ID AAV30137 standard; Protein: 817 AA.  
 XX  
 AC AAV30137;  
 XX  
 DT 27-OCT-1999 (first entry)  
 XX  
 DE Amino acid sequence of tumour suppressor protein NF- $\kappa$ B  
 XX  
 KW Nedasin, tumour suppressor protein, NF- $\kappa$ B, tumour suppression,  
 XX malignant tumour formation.  
 XX  
 OS Homo sapiens.  
 XX  
 PN W09943702-A1.  
 XX  
 PD 02-SEP-1999.  
 XX  
 PE 24-AUG-1998; 98WO-JP03740.  
 XX  
 PK 25-FEB-1998; 98JP-0043552.  
 XX  
 PA (SUMO) SUMITOMO ELECTRIC IND CO.  
 XX  
 PI Kishimoto T, Kuwahara H, Niwa S, Saya H,  
 XX  
 DR WPI: 1999-51845/73.  
 XX  
 DP N-PSDB: AAX85725.  
 XX  
 PT New nedasin protein, useful in the investigation of the mechanism of  
 XX formation of malignant tumours  
 XX  
 PS Example 1; Page 81-87; 104pp; Japanese.  
 XX  
 CC The present sequence represents tumour suppressor protein NF- $\kappa$ B. The  
 XX specification describes mammalian proteins, designated nedasin,  
 XX which bind to the tumour suppressor protein NF- $\kappa$ B. Nedasin is involved  
 XX with the regulation of tumour suppression mechanisms. Nedasin and  
 XX antibodies recognizing it are useful in the investigation of the  
 XX mechanism of formation of malignant tumours. The polynucleotides are  
 XX useful for screening cDNA libraries, and as a source of primers and  
 XX probes.  
 XX  
 SQ Sequence 817 AA;  
 XX  
 Query Match 17.4%; Score 203.5; DB:29; Length 817;  
 Best local Similarity 43.4%; Pred. No. 2e-11;  
 Matches 43; Conservative 18; Mismatches 37; Indels 1; Gaps 1;  
 QY 106 PAVVFLPKTFPGFENVWAKKQNSPIYSKIPQAVAFKSLKPKQULSNVSVES 155  
 DB 384 PRLILHKGSTGTYGRIYNG-EDGQGLTISLILAGPADLSGLTIGQTLISVAGNITRN 442  
 QY 166 EHHKFAVPIIKAKNSVKLVVYTPKVLKEMKPEKLR 204  
 DB 443 ALDGYATAIKRQSVTLVAGYRPGQYSRTSKINDIR 481  
 RESULT 11  
 ID AAW48102 standard; Protein: 849 AA.  
 XX  
 AC AAW48102;  
 XX  
 DT 15-JUN-1998 (first entry)  
 XX  
 DE Human discs large 1 gene-2 cancer related molecule.  
 XX  
 KW Human; NF- $\kappa$ B, discs large 1 gene, cancer related molecule, nerve,  
 XX internal secretion tissue.  
 XX  
 OS Homo sapiens.

XX  
 PN JP10066581-A.  
 XX  
 PD 10-MAR-1998.  
 XX  
 PE 23-AUG-1996; 96JP-0241370.  
 XX  
 PK 23-AUG-1996; 96JP-0241370.  
 XX  
 PA (SUMO) SUMITOMO ELECTRIC IND CO.  
 XX  
 DR WPI: 1998-224339/20.  
 XX  
 DP N-PSDB: AAV20420.  
 XX  
 PT Human discs large 1 gene family - useful in, e.g. therapeutic  
 XX composition(s) for treating cancer  
 XX  
 PS Claim 8; Page 18 20; 31pp; Japanese.  
 XX  
 CC The present sequence represents human dig 2 molecule. The present  
 XX invention describes human discs large 1 gene (dig) family expressible in  
 XX nerve tissue. Also described are: (1) a polynucleotide (PN) encoding dig  
 XX and comprising a 3100 (1) or 3213 bp (11) sequence; (2) RNA corresponding  
 XX to PN having sequences (1) and (11); (3) RNA having a base sequence  
 XX transcribed by dig; (4) an antisense PN having a at least 15 bp sequence,  
 XX and which is a part of PN of (1); (5) a derivative of the antisense PN;  
 XX (6) an antibody specific for dig; and (7) an antibody specific for a  
 XX polypeptide having a 817 or 849 aa sequence. The polypeptide, RNA's and  
 XX antibodies can be used for detection of dig. The antisense PN can be  
 XX used as a therapeutic composition for treating cancer.  
 XX  
 SQ Sequence 849 AA;  
 XX  
 Query Match 17.4%; Score 203.5; DB:19; Length 849;  
 Best local Similarity 43.4%; Pred. No. 2.2e-11;  
 Matches 43; Conservative 18; Mismatches 37; Indels 1; Gaps 1;  
 QY 106 PAVVFLPKTFPGFENVWAKKQNSPIYSKIPQAVAFKSLKPKQULSNVSVES 155  
 DB 384 PRLILHKGSTGTYGRIYNG-EDGQGLTISLILAGPADLSGLTIGQTLISVAGNITRN 442  
 QY 166 EHHKFAVPIIKAKNSVKLVVYTPKVLKEMKPEKLR 204  
 DB 443 ALDGYATAIKRQSVTLVAGYRPGQYSRTSKINDIR 481  
 RESULT 12  
 ID AAW34662 standard; Protein: 882 AA.  
 XX  
 AC AAW34662;  
 XX  
 DT 29-JUN-1998 (first entry)  
 XX  
 DE Partial PSD-93 protein sequence.  
 XX  
 KW PSD 93, GNG3, neuronal nitric oxide synthase, Alzheimer's disease,  
 XX diagnosis, muscular dystrophy, skeletal muscle, Huntington's disease;  
 KW Duchenne muscular dystrophy; Becker muscular dystrophy; dystrophin;  
 KW sarcotenuin; the domain; neurodegenerative disease; gene therapy;  
 XX amyotrophic lateral sclerosis.  
 XX  
 OS Rattus sp.  
 XX  
 PN W09733173-A1.  
 XX  
 PD 12-SEP-1997.  
 XX  
 PE 06-MAR-1997; 97WO-0304897.  
 XX  
 PK 06-MAR-1996; 96US-0613114.  
 XX



PD 23 MAY-2000. 2000WO-US14161.  
 XX  
 PR 12 MAY-2000; 2000WO-US14161.  
 XX  
 PR 14 MAY-1999; 990S-0144114.  
 PR 14 MAY-1999; 990S-0144117.  
 PR 14 MAY-1999; 990S-0144118.  
 PR 21 OCT-1999; 990S-0160860.  
 PR 29 OCT-1999; 990S-0162498.  
 PR 13 DEC-1999; 990S-0170453.  
 PR 14 JAN-2000; 2000US-0176195.  
 PR 14 FEB-2000; 2000US-0162296.  
 PR 11 APR-2000; 2000US-0164460.  
 PR 11 APR-2000; 2000US-0196527.  
 XX  
 PA (ARMO-) ARBOR VITA CORP.  
 XX  
 PI In PSI:  
 XX WPI: 2001-02-09/47703.  
 XX  
 PT Modulating a biological function of an endothelial cell or  
 PT hematopoietic cell, useful for treating autoimmune diseases and  
 PT infectious diseases, by administering an antagonist that inhibits  
 PT binding between a PDZ protein and a PL protein.  
 PS Disclosure: Page 28-43; 14pp; English.  
 XX  
 CC The present invention relates to a new method for modulating a  
 CC biological function of an endothelial cell or hematopoietic cell. The  
 CC method involves introducing into a cell, an antagonist that inhibits  
 CC binding between a PDZ protein and a PL protein. The inhibitor is used  
 CC to treat a disease mediated by hematopoietic cells, e.g., autoimmune  
 CC disease. It may also be used to prevent transplantation rejection of  
 CC a solid organ transplant. The method may also be used in the treatment  
 CC of inflammation, allergy, inflammatory bowel diseases, ulcerative  
 CC colitis, ileitis, psoriasis, asthma, atopic dermatitis, autoimmune  
 CC diseases (e.g., rheumatoid arthritis, multiple sclerosis,  
 CC insulin-dependent diabetes, Hashimoto thyroiditis, osteoarthritis,  
 CC graft rejection, transplantation rejection), atherosclerosis, strokes,  
 CC infectious diseases, ischemia, vasculitis and Crohn's disease.  
 XX  
 SO Sequence 97 AA:  
 Query Match 40.38; Score 472; Dh 22; Length 97;  
 Best local Similarity 100.0%; Prod. No. 1.8e-19; Indels 0; Gaps 0;  
 Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 103 HSHPRVVLPTPTETGHNVMGTFQNSPIYISPIIPQZVAEPHGLKPGQQLSYNCVS 162  
 DB 1 LSHPRVVLPTPTETGHNVMGTFQNSPIYISPIIPQZVAEPHGLKPGQQLSYNCVS 60  
 QY 163 VGEHHEKAVELAKAKDSVKLVVRYTPKYLE 194  
 DB 61 VGEHHEKAVELAKAKDSVKLVVRYTPKYLE 92  
 DE 61 VGEHHEKAVELAKAKDSVKLVVRYTPKYLE 92  
 XX  
 DE Tax interaction protein 33 PDZ domain.  
 XX  
 KW Endothelial cell; hematopoietic cell; PDZ domain protein;  
 KW PL domain protein; leukocyte activation; synapse formation;  
 KW transmembrane neurotransmitter receptor; autoimmune disease;  
 KW transplantation rejection; inflammation; allergy;  
 KW inflammatory bowel disease; ulcerative colitis; ileitis; psoriasis;

KW asthma; atopic dermatitis; atherosclerosis; cancer; infectious disease;  
 KW Ischemia; vasculitis; Crohn's disease.  
 XX  
 OS Homo sapiens.  
 PN W0200065897-A2.  
 XX  
 PD 23 MAY-2000.  
 XX  
 PR 12 MAY-2000; 2000WO-US14166.  
 XX  
 PR 14 MAY-1999; 990S-0144114.  
 PR 14 MAY-1999; 990S-0144117.  
 PR 14 MAY-1999; 990S-0144118.  
 PR 21 OCT-1999; 990S-0160860.  
 PR 29 OCT-1999; 990S-0162498.  
 PR 13 DEC-1999; 990S-0170453.  
 PR 14 JAN-2000; 2000US-0176195.  
 PR 14 FEB-2000; 2000US-0162296.  
 PR 11 APR-2000; 2000US-0164460.  
 PR 11 APR-2000; 2000US-0196527.  
 XX  
 PA (ARMO-) ARBOR VITA CORP.  
 XX  
 PI In PSI:  
 XX WPI: 2001-02-09/47703.  
 XX  
 PT New inhibitors of binding of a PDZ protein and PL protein for  
 PT inhibiting a cell-mediated response by hematopoietic cells, or for  
 PT treating diseases characterized by inflammatory and humoral immune  
 PT responses, e.g., inflammation, cancer.  
 PS Disclosure: Page 30; 13pp; English.  
 XX  
 CC The present invention relates to a method for modulating a biological  
 CC function of an endothelial cell or hematopoietic cell, comprises  
 CC introducing into a cell an antagonist that inhibits binding between a  
 CC PDZ domain protein and a PL domain protein to result in inhibition of  
 CC a cell-mediated response. The present sequence is a PDZ domain. PDZ domains  
 CC or proteins are named after three prototypal proteins: PSD95,  
 CC Drosophila large disc protein and Zonula Occludin 1 protein. PDZ domain  
 CC proteins are involved in synapse formation by organized transmembrane  
 CC neurotransmitter receptors through intracellular interactions. The  
 CC inhibitors identified by the present invention can be used to treat a  
 CC disease mediated by hematopoietic cells, e.g., autoimmune disease,  
 CC inflammation, allergy (e.g., drug allergies), inflammatory bowel diseases,  
 CC ulcerative colitis, ileitis, psoriasis, respiratory allergic diseases  
 CC (e.g., asthma), atopic dermatitis, autoimmune diseases (e.g., rheumatoid  
 CC arthritis, multiple sclerosis), insulin dependent diabetes, Hashimoto  
 CC thyroiditis, osteoarthritis), atherosclerosis, cancers, infectious  
 CC diseases (e.g., graft rejection), ischemia, vasculitis and Crohn's  
 CC disease. The inhibitors can also be used to prevent transplantation  
 CC rejection of a solid organ transplant.  
 XX  
 SO Sequence 97 AA:  
 Query Match 40.38; Score 472; Dh 22; Length 97;  
 Best local Similarity 100.0%; Prod. No. 1.8e-19; Indels 0; Gaps 0;  
 Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 103 HSHPRVVLPTPTETGHNVMGTFQNSPIYISPIIPQZVAEPHGLKPGQQLSYNCVS 162  
 DB 1 LSHPRVVLPTPTETGHNVMGTFQNSPIYISPIIPQZVAEPHGLKPGQQLSYNCVS 60  
 QY 163 VGEHHEKAVELAKAKDSVKLVVRYTPKYLE 194  
 DB 61 VGEHHEKAVELAKAKDSVKLVVRYTPKYLE 92  
 DE 61 VGEHHEKAVELAKAKDSVKLVVRYTPKYLE 92  
 XX  
 DE Tax interaction protein 33 PDZ domain.  
 XX  
 KW Endothelial cell; hematopoietic cell; PDZ domain protein;  
 KW PL domain protein; leukocyte activation; synapse formation;  
 KW transmembrane neurotransmitter receptor; autoimmune disease;  
 KW transplantation rejection; inflammation; allergy;  
 KW inflammatory bowel disease; ulcerative colitis; ileitis; psoriasis;



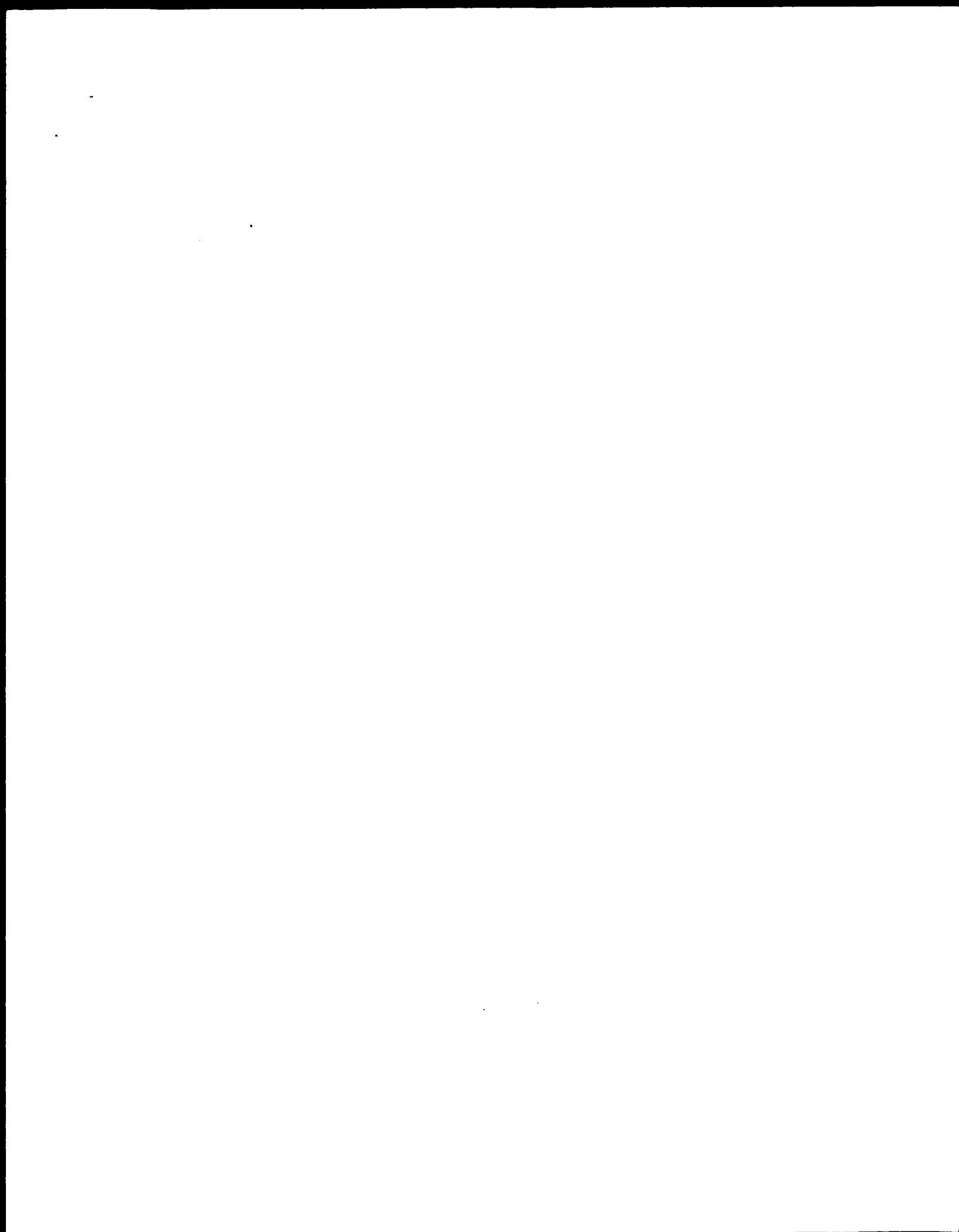
[illegible]

IN W1200069876 AZ  
XX













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UY 144 ISRLIPGVAPRHSLEKPKVSLISVGVSVLGGSEHFAVETLFAAGSVETIVSTPVL 193
DB 119 ISRLIPGVAPRHSLEKPKVSLISVGVSVLGGSEHFAVETLFAAGSVETIVSTPVL 178
UY 194 EEMFAEFKELTAPPE 209
DB 179 EEMFAEFKELTAPPE 194
RESULT 9
AC 092251 PPT:IMINARY PRT: 192 AA.
DI 01-MAY-1999 (FIRMREL: 19, created)
DI 01-MAY-1999 (FIRMREL: 19, last sequence update)
DI 01-JUN-2001 (FIRMREL: 17, last annotation update)
DB LIN-7A.
US Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Grahiata; Vertebrata; Euteostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OC NCBI_TaxId=10116.
AN 111
RP SEQUENCE FROM N.A.
KA Irie M., Hata Y., Deguchi M., Ise N., Hirao K., Yao I., Nishioke H.,
KA Takai Y.
RT "Isolation and Characterization of Mamalian Homologues of
RT Caenorhabditis elegans Lin-7, Localization at Cell-Cell Junction."
RT Oncogene 0:0-0(1999).
DB EMBL: AF090144; AAC78074.1; -.
DB HSSP: 012923; 4092.
DB InterPro: IPR001478; PDZ.
DB Pfam: PF00595; PDZ_1.
DB SMART: SM00228; PDZ_1.
DB PROSITE: PS01062; PDZ_1.
DB PROSITE: PS01062; PDZ_1.
DB SEQUENCE 192 AA: 19927 MW: 194839055.108 GRC64.

Query Match 64.8%, Score 758, DB 11, Length 182,
Best Local Similarity 98.78; Pred. No. 1,66-50;
Matches 149; Conservative 2; Mismatches 0; Indels 0; Gaps 0.

UY 14 MATLVVQPLIDPVAPAPLIPKIDPSGEVPHLQSLAKVLSHPVTAKEVYVYGM 73
DB 1 MATLVVQPLIDPVAPAPLIPKIDPSGEVPHLQSLAKVLSHPVTAKEVYVYGM 60
UY 74 ETTVNGGPEPPAPATATVAAFAAPSPGSPVPVPIPTREPGTGFVNMGGKGNPSLY 133
DB 61 ETTVNGGPEPPAPATATVAAFAAPSPGSPVPVPIPTREPGTGFVNMGGKGNPSLY 120
UY 134 ISRLIPGVAPRHSLEKPKVSLISVGVSVLGGSEHFAVETLFAAGSVETIVSTPVL 193
DB 121 ISRLIPGVAPRHSLEKPKVSLISVGVSVLGGSEHFAVETLFAAGSVETIVSTPVL 178
RESULT 10
AC 092251 PPT:IMINARY PRT: 195 AA.
DI 01-MAY-2000 (FIRMREL: 13, created)
DI 01-MAY-2000 (FIRMREL: 13, last sequence update)
DI 01-JUN-2001 (FIRMREL: 17, last annotation update)
DB G67662 PROTEIN
DB VESTOR G67662.
US Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Insecta; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Musciformia;
OC Ephydroidea; Drosophilidae; Drosophila.
OC NCBI_TaxId=7227.
AN 111
RP SEQUENCE FROM N.A.
KA STRAIN BEKLEY.
DB MEDLINE: 20196006; PubMed 10731132.

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KA Adams M.D., Celisner S.E., Holt R.A., Evans G.A., Gocayne J.D.,
KA Arachis F.S., Chaker S.E., Li P.W., Beckius E.A., Zille E.F.,
KA George K.A., Lewis S.E., Richards S., Ashburner M., Bradshaw S.N.,
KA Fulton G.G., Wolfman J.R., Yandell M.D., Zhang Q., Chen L.X.,
KA Brannon R.C., Rogers Y.-H.C., Blazek R.G., Champe M., Pfeiffer B.D.,
KA Wan K.H., Doyle S., Baxter E.C., Bell S., Nelson G.R., Miklos G.L.D.,
KA April J.P., Aubert A., An H., Andrews Pankoth C., Baldwin D.,
KA Balow R.M., Basu A., Baxendale J., Boykatalovich I., Brasley E.M.,
KA Brown K.Y., Brown P.V., Bernan B.P., Bhattacharya D., Bolshakov S.,
KA Borokova D., Botchan M.R., Bouck J., Brokstein P., Bruttner P.,
KA Burris K.C., Busam D.A., Butler H., Gaddipati K., Genter A., Chandra T.,
KA Cherry J.M., Cawley S., Dahlke G., Davaport L.H., Davies P.,
KA De Felice H., Decker A., Deitz E., May A.D., Lee T., Dietz G.M.,
KA Dierker N.L., Harvey D., Helman T.J., Hertzberg J.P., Hertz J.,
KA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ikegami G.,
KA Jialili M., Kalash P., Karpen G.B., Ko Z., Kennison J.A., Kothiyar K.A.,
KA Kramel R.E., Kodira G.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
KA Lasko F., Lee Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
KA Liu X., Mallet R., McIntosh T.C., McKay M.P., McPherson D.,
KA Markovoy G., Mishina N.V., Mobarry C., Morris J., Moshir A.,
KA Meek S.M., Mey M., Murphy D., Murphy M., Murty D.M., Nelson D.L.,
KA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacht J.M.,
KA Palacios H., Pittman K.S., Pan S., Pfland J., Puri V., Reese M.G.,
KA Reinert K., Rimmington K., Saunders R.D.C., Schneider M.P., Shen H.,
KA Shue R.C., Sidor-Kiamis L., Simpson M., Sirota M.P., Smith T.,
KA Spier E., Spradling A.C., Stapleton M., Stroud K., Sun E.,
KA Swickas R., Tector G., Turner R., Venter E., Wang A.H., Wang X.,
KA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
KA Williams S.M., Woodard T., Wolley K.C., Wu D., Yang S., Yao Q.A.,
KA Ye J., Yeh E.F., Yang S., Yang S., Yang S., Yang S., Yang S.,
KA Zhang X.H., Zhang F.R., Zhang F.R., Zhang X., Zhang X., Zhang X.,
KA Gibbs R.A., Myers E.W., Rubin G.B., Venter J.C.,
RT "The genome sequence of Drosophila melanogaster."
DB EMBL: AF081750; AAF56389.1; -.
DB HSSP: 012959; 1098.
DB InterPro: IPR0009269; cell.
DB Pfam: PF001478; PDZ.
DB SMART: SM00228; PDZ_1.
DB PROSITE: PS01062; PDZ_1.
DB PROSITE: PS01062; PDZ_1.
DB SEQUENCE 195 AA: 21493 MW: 89058717.3780 GRC64.

Query Match 64.48%, Score 754, DB 5, Length 195,
Best Local Similarity 77.94; Pred. No. 4, 50-50;
Matches 118; Conservative 20; Mismatches 22; Indels 0; Gaps 0.

UY 21 GRTTTEGVAPVLTLELGEVFTVPHFTGTPVVFSTFGTAPVYVYMHFTTVNG 80
DB 6 GRTTTEGVAPVLTLELGEVFTVPHFTGTPVVFSTFGTAPVYVYMHFTTVNG 65
UY 81 GRTTTEGVAPVLTLELGEVFTVPHFTGTPVVFSTFGTAPVYVYMHFTTVNG 140
DB 66 SHHWASATATATVAAFAAPSPGSPVPVPIPTREPGTGFVNMGGKGNPSLY 125
UY 111 GYALHDTFGTGLGVNVGVSVLGGSEHFAVETLFAAGSVETIVSTPVL 209
DB 126 GYALHDTFGTGLGVNVGVSVLGGSEHFAVETLFAAGSVETIVSTPVL 185
UY 201 EKLTAEPKQ 210
DB 186 EKLTAEPKQ 195
RESULT 11
AC 090245 PPT:IMINARY PRT: 317 AA.
DI 090245
DB MEDLINE: 20196006; PubMed 10731132.

```



RL 0-11 94:773-782(1998).  
 RN 121  
 RE SEQUENCE FROM N.A.  
 RX MEDLINE:99274734 PubMed:1041123  
 RA JO K., Dohm R., Li M., Hredt D.S.  
 R1 Characterization of MAI-8/9/10/11/12/13/14/15/16/17 homologs enriched at brain synapses in association with the postsynaptic density of Drosophila ommatidia. *Development* 126:111-121 (1999).  
 R1 J. Neurosci. 19:4189-4196(1999).  
 RK EMBL: AF0087604 AAC29482.1  
 RL EMBL: AF173082 AAC48501.1  
 DR HSSP: Q12923 40%.  
 DR MDJ: M611340864 V0112.  
 DR InterPro: IPR001478; PDZ.  
 DR Pfam: PF00595; PDZ-1.  
 DR SMART: SM00226; PDZ-1.  
 DR PROSITE: PS50106; PDZ-1.  
 SE SEQUENCE 207 AA: 22914 MW: 1656679486.89F03 CR064;

Query Match 69.08; Score 807; DR 11; Length 207.  
 Host Local Similarity 79.18; Pred. No. 2,16-54;  
 Matches 157; Conservative 24; Mismatches 15; Indels 2; Gaps 1;

QY 14 MATTVVAPITTPDVAAPETLPTVESEVAVKLSLKEVSEPTATREYVYAH 74  
 111 111 111 111 111 111 111 111 111 111 111 111 111 111 111  
 DB 1 MAAL--VRI--GIRVSAVAVTLPRLGPRSLDRLDTALDVLQSPRSATREYVY 58  
 QY 74 ETTVVGTRERVAATATVAATAASEGSHRVVLTGRTGSLGFRWAGEKSTLY 133  
 111 111 111 111 111 111 111 111 111 111 111 111 111 111 111  
 DB 59 ETTTTSVAVRVAATATVAATAASEGSHRVVLTGRTGSLGFRWAGEKSTLY 118  
 QY 134 ISKIPKSAVAFHSLKRPDLTSVNVSVSPRENEKAVPLKAMISVLELVYPRVYL 193  
 111 111 111 111 111 111 111 111 111 111 111 111 111 111 111  
 DB 119 ISVLEKGVAVHSLKRPDLTSVNVSVSPRENEKAVPLKAMISVLELVYPRVYL 178  
 QY 194 FPMARFPRKLTARPOO 211  
 111 111 111 111 111 111 111 111 111 111 111 111 111 111 111  
 DB 179 FPMARFPRKMSARPOO 195  
 RESULT 7  
 QYHAP6 PRELIMINARY PRI: 207 AA.  
 AN QYHAP6  
 BT 01-MAR-2001 (TRIMBL: 15, Created)  
 BT 01-MAR-2001 (TRIMBL: 16, last sequence update)  
 BT 01-JUN-2001 (TRIMBL: 17, last annotation update)  
 DE LIN-78.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
 ON NCBI:taxid:9606;  
 RN 111  
 RE SEQUENCE FROM N.A.  
 RP TISSUE: KIDNEY.  
 RA Jensen O., Liu H., Merot J., Welling P.A.  
 R1 "Basolateral Membrane Expression of the Kir 2.3 Channel is Coordinated by a Piv Interaction with Lin-7/ANKK".  
 R1 Submitted (oct-2000) to the EMBL database.  
 DR EMBL: AF11862; AAC34117.1  
 DR InterPro: IPR001478; PDZ.  
 DR Pfam: PF00595; PDZ-1.  
 DR SMART: SM00226; PDZ-1.  
 DR PROSITE: PS50106; PDZ-1.  
 SE SEQUENCE 207 AA: 22896 MW: 631890827069800 CR054;

Query Match 69.08; Score 807; DR 4; Length 207.  
 Host Local Similarity 78.58; Pred. No. 4,46-54;  
 Matches 157; Conservative 24; Mismatches 15; Indels 2; Gaps 1;

RL 0-11 111 111 111 111 111 111 111 111 111 111 111 111 111 111  
 RN 1 MAAL--VRI--GIRVSAVAVTLPRLGPRSLDRLDTALDVLQSPRSATREYVY 58  
 QY 74 ETTVVGTRERVAATATVAATAASEGSHRVVLTGRTGSLGFRWAGEKSTLY 133  
 111 111 111 111 111 111 111 111 111 111 111 111 111 111 111  
 DB 59 ETTTTSVAVRVAATATVAATAASEGSHRVVLTGRTGSLGFRWAGEKSTLY 118  
 QY 134 ISKIPKSAVAFHSLKRPDLTSVNVSVSPRENEKAVPLKAMISVLELVYPRVYL 193  
 111 111 111 111 111 111 111 111 111 111 111 111 111 111 111  
 DB 119 ISVLEKGVAVHSLKRPDLTSVNVSVSPRENEKAVPLKAMISVLELVYPRVYL 178  
 QY 194 FPMARFPRKLTARPOO 211  
 111 111 111 111 111 111 111 111 111 111 111 111 111 111 111  
 DB 179 FPMARFPRKMSARPOO 195  
 RESULT 8  
 QYHAP6 PRELIMINARY PRI: 244 AA.  
 AN QYHAP6  
 BT 01-JUN-2001 (TRIMBL: 17, Created)  
 BT 01-JUN-2001 (TRIMBL: 17, last sequence update)  
 BT 01-JUN-2001 (TRIMBL: 17, last annotation update)  
 DE VERTEBRATE HOMOLOG OF C. ELKANS LIN-7 TYPE 2.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 ON NCBI:taxid:10090;  
 RN 111  
 RE SEQUENCE FROM N.A.  
 RP STRAIN G57H/66; TISSUE:HIPPOCAMPUS;  
 RX MEDLINE:2106760; PubMed:11217851;  
 RA Kawai J., Shimaoka A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
 ARK923.1, Hara A., Takahashi Y., Kame H., Aizawa K., Ikeda S.,  
 RA Aizawa K., Ikeda S., Nishi K., Kiyosawa H., Kondo S., Yamada K.,  
 RA Saito T., Okazaki Y., Gotoh T., Kato H., Kasakawa T., Saito R.,  
 RA Kato A. K., Matsuda H. A., Ashburner M., Farafar S., Gassan T.,  
 RA Felschmann W., Gaudelund T., Gissi G., Lind B., Koshida H.,  
 RA Koehl P., Lewis S., Matsuo Y., Nikaido I., Paoletti G., vanKubuski J.,  
 RA Schirral L. M., Staudl F., Suzuki R., Tomita M., Watanabe T.,  
 RA Sakai K., Okido T., Purjono M., Aono H., Baldarelli R., Barsh G.,  
 RA Blake J., Bottelli D., Bojunga N., Gattolusi P., de Beldade M.F.,  
 RA Bismuth M., Bull C., Fietcher C., Fujita M., Gariboldi M.,  
 RA Gustlich S., Hill D., Holmann M., Hume D.A., Kamiya M., Lee N.H.,  
 RA Lyons J., Marchionni D., Mashima M., Mazzarelli J., Mubareks P.,  
 RA Nordone P., Pina R., Ringwald M., Rodriguez I., Sakamoto N.,  
 RA Sasai H., Sato K., Sengler C., Seng T., Shibata Y., Smith K. R.,  
 RA Suzuki H., Taya O. K., Wada K. H., Weller G., Willeker G., Wilting L.,  
 RA Wyszynski A., Yoshida Y., Yasuda Y., Kawasaki H., Yoshida S.,  
 RA Wyszynski A.  
 R1 "Functional annotation of a full-length mouse cDNA collection".  
 RL Nature 409:685-690(2001).  
 DR EMBL: AK019299; BA81655.1  
 DR MDJ: M611340858; V0112.  
 DR InterPro: IPR001478; PDZ.  
 DR Pfam: PF00595; PDZ-1.  
 DR SMART: SM00226; PDZ-1.  
 DR PROSITE: PS50106; PDZ-1.  
 SE SEQUENCE 244 AA: 25732 MW: 769198812396548 CR064;

Query Match 68.38; Score 799; DR 11; Length 244;  
 Host Local Similarity 79.18; Pred. No. 1,66-58;  
 Matches 155; Conservative 24; Mismatches 15; Indels 2; Gaps 1;

QY 14 MATTVVAPITTPDVAAPETLPTVESEVAVKLSLKEVSEPTATREYVYAH 74  
 111 111 111 111 111 111 111 111 111 111 111 111 111 111 111  
 DB 1 MAAL--VRI--GIRVSAVAVTLPRLGPRSLDRLDTALDVLQSPRSATREYVY 58  
 QY 74 ETTVVGTRERVAATATVAATAASEGSHRVVLTGRTGSLGFRWAGEKSTLY 133  
 111 111 111 111 111 111 111 111 111 111 111 111 111 111 111  
 DB 59 ETTTTSVAVRVAATATVAATAASEGSHRVVLTGRTGSLGFRWAGEKSTLY 118













QY 213 QULLQ 217  
DB 583 SLVVR 589

## RESULT 10

156552  
Synapso-associated protein 97 - rat  
CSpecies: Rattus norvegicus (R. norvegicus)  
CDate: 26 Jul 1996 #sequence\_revision 26 Jul 1996 #text\_change 21 Jan 2000  
CAccession: 156552  
R.Muller, B.M.J. Kistner, U.J. Veb, R.W.J. Cases-Langhoff, G.J. Becker, B.J. Gundelfinger, R.J. Neufussel, 15, 2354-2366, 1995  
A>Title: Molecular characterization and spatial distribution of SAP97, a novel presynaptic  
A.Reference number: 156552; M010-95198112  
A:Accession: 156552  
A>Status: preliminary; translated from cDNA/EMBL/GenBank

A:Molecule type: mRNA  
A:Residues: 1-911 - RESs  
A:Cross references: EMBL:U11450; NIDB:13455; PIR:AA79976.1; FID:61345  
C:Similarity: disc-large tumor suppressor disc domain homology, guanylate kinase hom  
E:229 307/49-mut - 90% domain homology 90%  
E:423 407/49-mut - 80% domain homology 80%  
E:587-645/49-mut - 80% domain homology 80%  
E:722-839/49-mut - 100% domain homology 100%

Query Match 16.4% Score 192; DB 2; Length 911;  
Best Local Similarity 45.2% Prod. No. 1-30-06;

Matches 44; Conservation 23; Mismatches 44; Indels 11; Gaps 2;  
QY 106 PRVVLKTKDEGFVNVKSPKNSVYISLLEKVALEHDLKPKVILSVNCSVEG 165  
DB 463 PRVVLHPSVIGLGNVWQ-FPGEPHISPIAAMDAMSPKPPHISVNVGLPA 521

QY 166 EHHKAVALLAAKESVAVVETVILVLEKAEKLEK-----TARRKQC 212  
DB 522 ASHEQAAALAKNGLAV IVALPPPVSPFAPKIRIPVIMNSVSSGSLPSPFP 591

QY 213 QULLQ 217  
DB 583 SLVVR 589

## RESULT 11

148756  
homolog of Drosophila discs-large protein, isoform 2 - human  
CSpecies: Homo sapiens (man)  
CDate: 31 Mar 1996 #sequence\_revision 31 Mar 1996 #text\_change 21 Jan 2000  
CAccession: 148756  
Raine, R.A.; Marfatia, S.M.; Branton, D.; Chishti, A.H.  
Proc. Natl. Acad. Sci. U.S.A. 91, 9818-9822, 1994  
A>Title: Cloning and characterization of hdlg, the human homologue of the Drosophila disc  
A.Reference number: 148756; M010-95024052  
A:Accession: 148756  
A>Status: preliminary

A:Molecule type: mRNA  
A:Residues: 1-926 - RESs  
A:Cross references: EMBL:U01896; NIDB:58435; PIR:AA69596.1; FID:458436  
C:Genetics:  
A:Gene: DDL1  
A:Gene: DDL1  
A:Cross references: cDNA/EMBL/GenBank  
A:Map position: 4q29-q29  
C:Similarity: disc-large tumor suppressor disc domain homology, guanylate kinase hom  
E:229-307/49-mut - 90% domain homology 90%  
E:423-407/49-mut - 80% domain homology 80%  
E:587-645/49-mut - 80% domain homology 80%  
E:722-839/49-mut - 100% domain homology 100%

Query Match 16.4% Score 192; DB 2; Length 926;

Best Local Similarity 45.2% Prod. No. 1-30-06;  
Matches 44; Conservation 23; Mismatches 44; Indels 11; Gaps 2;

QY 106 PRVVLKTKDEGFVNVKSPKNSVYISLLEKVALEHDLKPKVILSVNCSVEG 165  
DB 463 PRVVLHPSVIGLGNVWQ-FPGEPHISPIAAMDAMSPKPPHISVNVGLPA 521

QY 166 EHHKAVALLAAKESVAVVETVILVLEKAEKLEK-----TARRKQC 212  
DB 522 ASHEQAAALAKNGLAV IVALPPPVSPFAPKIRIPVIMNSVSSGSLPSPFP 591

QY 213 QULLQ 217  
DB 583 SLVVR 589

## RESULT 12

130259  
multiple P02 domain protein - mouse  
CSpecies: Mus musculus (house mouse)  
CDate: 29 Oct 1999 #sequence\_revision 29 Oct 1999 #text\_change 21 Jan 2000  
CAccession: 130259  
E:Sting, C.F. Boz, C.J. Boz, B. Jackson, J.D.  
Genomics 29, 102-104, 1999  
A>Title: Identification, sequencing and mapping of mouse multiple P02 domain protein 9  
A.Reference number: 130259; M010-95024052  
A:Accession: 130259  
A>Status: preliminary; translated from cDNA/EMBL/GenBank

A:Molecule type: mRNA  
A:Residues: 1-2055 - RESs  
A:Cross references: EMBL:AF11863; NIDB:94153877; FID:7041523.1; FID:94153878

A:Experimental source: strain C57BL/6 x DBA/2J whole brain  
C:Genetics:  
A:Gene: mpd2  
A:Map position: 4

Query Match 16.4% Score 191.5; DB 2; Length 2055;  
Best Local Similarity 29.0% Prod. No. 3-70-06;

Matches 56; Conservation 31; Mismatches 81; Indels 25; Gaps 4;

QY 1 MKRVSIAPIADMAI---ITVQGLILDRVAVILILEKIDPSKGVVHKIKSKV 56  
DB 1879 MKRIRVVAQLTKIISVGRVITIGSTIGMTHGLAVNPKASQSLVGVVAADVSV 1938

QY 57 LQSECTAIKEVYVMEITIVNGEPKAPATAKATVAAFAASGSHPPVVELPKIDE 116  
DB 1939 LQ-----HGEFLANPCLAF---TGTSSSLPPIQDGPSSKILIDKQPD 1980

QY 117 LELIIRMLL KLDSI DLEPLDGLVAFKGLKGLKLSVAVVILHETAVE 173  
DB 1981 GLSFNIVGVGSPHGLPIYKTVAKGVAAEGLKQDGLIIVNGLSLRVTHERAVA 2040

QY 174 LKFAVSVGLV 186  
DB 2041 LKTKKIVTLMV 2054

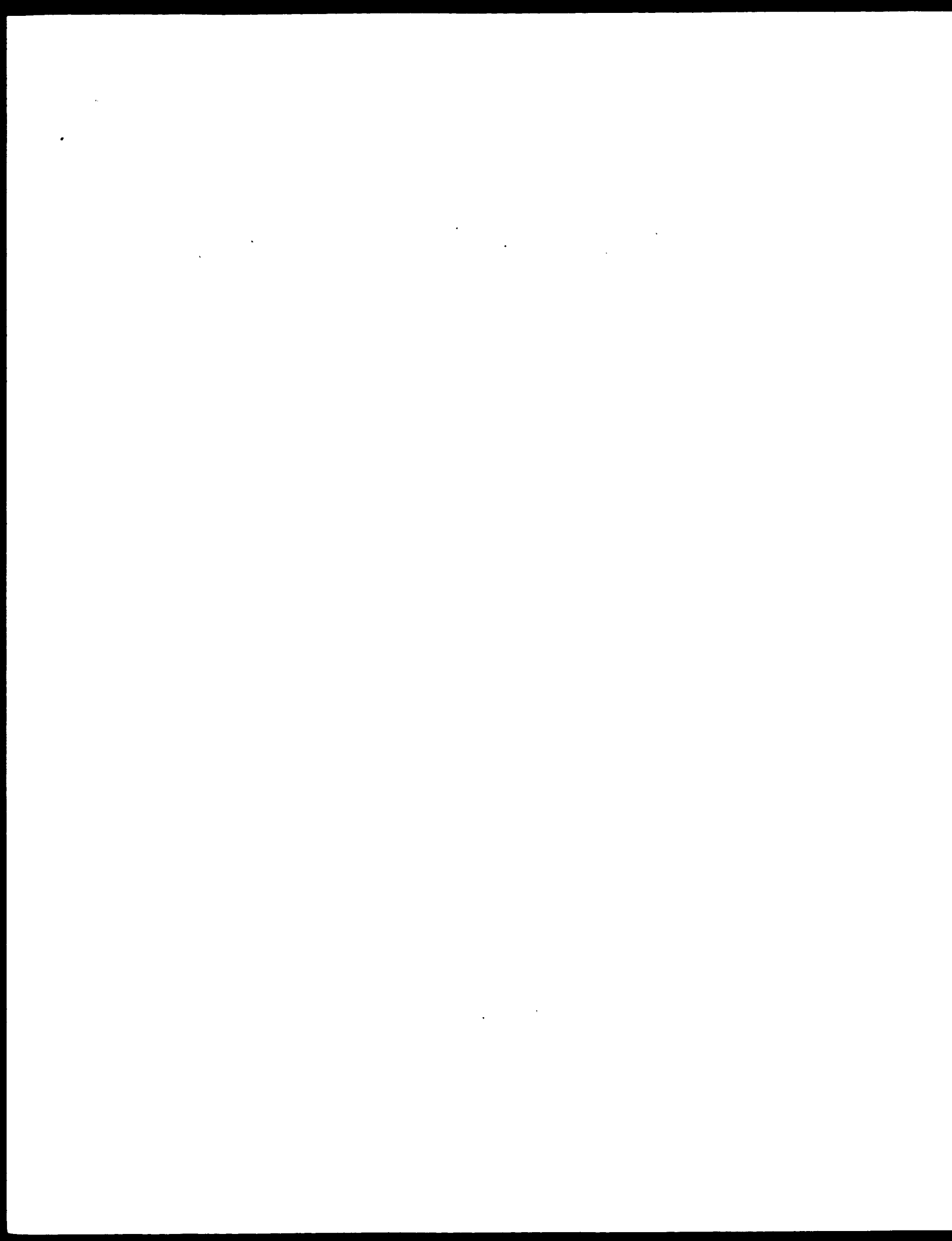
## RESULT 13

146612  
multi P02 domain protein 1 - rat  
CSpecies: Rattus norvegicus (Norway rat)  
CDate: 18 Feb 2000 #sequence\_revision 18 Feb 2000 #text\_change 21 Jan 2000  
CAccession: 146612  
R.Muller, B.M.J. Kistner, U.J. Veb, R.W.J. Cases-Langhoff, G.J. Becker, B.J. Gundelfinger, R.J. Neufussel, 15, 2354-2366, 1995  
A>Title: Cloning and characterization of SAP97, a novel disc domain protein.  
A.Reference number: 223104; M010-98196865  
A:Accession: 146612  
A>Status: preliminary; translated from cDNA/EMBL/GenBank

A:Molecule type: mRNA  
A:Residues: 1-2054 - RESs  
A:Cross references: EMBL:AF061720; NIDB:4295929; PIR:AA69601.1; FID:4295929











DE LEPHAL(1)DISCS LARGE-1 TUMOR SUPPRESSOR PROTEIN.  
GN Dlg1.  
OS Drosophila melanogaster (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
OC Euryptera; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephydriidae; Ephydriidae; Ephydriidae; Ephydriidae;  
KN NBL\_taxid=7227;  
RN [1]  
RX MEDLINE=9130294; PubMed=1651169;  
KA Woods D.F., Bryant P.J.;  
PI "the discs large tumor suppressor gene of Drosophila encodes a  
quanylate kinase homolog localized at septate junctions.";  
RL Cell 66:451-464(1991).  
CC -1- FUNCTION: LOSS OF THIS PROTEIN CAUSES LARGE IMAGINAL DISCS BY  
ALUMINUM NEOPLASTIC OVERGROWTH. THE PRESENCE OF A GUANYLATE KINASE  
DOMAIN SUGGESTS INVOLVEMENT IN ADOQUATE CELLULAR ADHESION AS WELL  
AS SIGNAL TRANSDUCTION TO CONTROL CELLULAR PROLIFERATION. THE DLG  
PROTEIN PLAYS A CRITICAL ROLE AT SEPTATE JUNCTIONS IN CELLULAR  
GROWTH CONTROL DURING LARVAL DEVELOPMENT.  
CC -1- SUBCELLULAR LOCATION: CYTOSKELETON-ASSOCIATED. LOCATED AT THE  
CYTOSOL/FACIAL FACE OF THE MEMBRANE IN THE CELLULAR BLASTODERM AND  
BECOMES ASSOCIATED WITH SEPTATE JUNCTIONS WHICH BEGIN TO FORM  
BETWEEN EPITHELIAL CELLS AT THE TIME OF DORSAL CLOSURE. IN ADULT  
FLIES, LOCATED AT THE APICAL-LATERAL MEMBRANE BOUNDARY OF  
EPITHELIAL CELLS.  
CC -1- ALTERNATIVE PRODUCTS: LEADS TO DIFFERENT FORMS OF THE PROTEIN;  
THE SEQUENCE SHOWN REFERS TO THE FLO-A PROTEIN, THAT IS MOST  
ABUNDANTLY EXPRESSED.  
CC -1- TISSUE SPECIFICITY: ABUNDANTLY EXPRESSED IN  
EPITHELIAL TISSUES. DEVELOPMENTAL STAGE DEPENDENT EXPRESSION.  
CC -1- SIMILARITY: CONTAINS 3 PDZ/DHR DOMAINS  
CC -1- SIMILARITY: CONTAINS A GUANYLATE KINASE-LIKE DOMAIN.  
CC -1- SIMILARITY: BELONGS TO THE MAGOK FAMILY OF CELL JUNCTION PROTEINS.  
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CC  
CC FMBL: M73529; AAA28468.1;  
CC EMBL: A39651; A39651.  
CC HSSP: Q12959; IPDR.  
CC P1phase: PFM0001624; dly1.  
CC InterPro: IPR000619; Guanylate\_kin.  
CC InterPro: IPR001478; PDZ.  
CC InterPro: IPR001452; SH3.  
CC Pfam: PF00625; Guanylate\_kin; 1.  
CC Pfam: PF00795; PDZ; 3.  
CC Pfam: PF00018; SH3; 1.  
CC SMART: SM00072; GUKC; 1.  
CC SMART: SM00228; PDZ; 3.  
CC SMART: SM00326; SH3; 1.  
CC PROSITE: PS00856; GUANYLATE\_KINASE\_1; 1.  
CC PROSITE: PS00952; GUANYLATE\_KINASE\_2; 1.  
CC PROSITE: PS0106; PDZ; 3.  
CC PROSITE: PS00002; SH3; 1.  
CC Trasnucore: SH3 domain; Alternative splicing: Repeat.  
CC K1 domain: 40 126 PDZ 1.  
CC E1 domain: 154 244 PDZ 2.  
CC F1 domain: 486 566 PDZ 3.  
CC F1 domain: 600 670 SH3.  
CC F1 domain: 768 960 SH3.  
CC SpliceSite: 960 AA; 102468 MW; BF87A422PFB6A5 CRO64;  
Query Match: 17 8%; Score 208.5; DB 1; Length 963;  
Best Local Similarity: 39.3%; Pred. No. 1e-07;  
Matches: 46; Conservative: 21; Mismatches: 49; Indels: 1; Gaps: 1;

QY 88 ATAAIAAARASCHSHREVELEPTDGLCHRWGCKGNSPTITSLINCAVATK 147  
DB 466 AVPTGPAVSTFETTPETITGKPAQCHENIV93-FPGAGIVSPFLIMACHVADLS 524  
CC 148 TFFPCTGCVNVEVEGTFHREAVALLRAAHLSTLVAVYVGHVLEHLEAAAL 204  
DB 525 EIKRGDGLISVNNVNLTHAHERAAALAKISGVVILLVQYREHYNKEFAALDEIK 581  
RESULT 4  
ID Dlg3\_HUMAN STANDARD: PRI: 817 AA.  
AC Q92796; Q90L18;  
DT 01-NOV-1997 (rel. 35, last sequence update)  
DT 01-NOV-1997 (rel. 35, last sequence update)  
DT 20-AUG-2001 (rel. 40, last annotation update)  
DE PRESYNAPTIC PROTEIN SAP102 (SYNAPSE-ASSOCIATED PROTEIN 102)  
DE (NEUROKININ-2/3) (NE Dlg) (DISCS, LARGE HOMOLOG 3).  
GN Dlg3 Or KIAA1232.  
OS Homo sapiens (human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eumetazoa; Mammalia; Eularchia; Primates; Catarrhini; Hominoidea; Homo.  
OC Musculi; Embryos; Fetuses; Cerebrum; Homoides; Homo.  
OX NCB1\_taxid=9606;  
RN [1]  
RX MEDLINE=9732623; PubMed=9188857;  
RA Mavroto F., Pouchard H., Masuho H., Nishiyama Y., Morisaki T.,  
RA Sasaki J., Nakao M., Kuwano A., Nakata M., Ushio Y., Saito H.;  
RT "Cloning and characterization of NE-dlg, a novel human homolog of the  
RT Drosophila discs large (dlg) tumor suppressor protein interacts with  
RL the APC protein.";  
RL Oncogene 14:2425-2433(1997).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Fetal brain;  
RX MEDLINE=9732623; PubMed=9188857;  
RA Mavroto F., Pouchard H., Masuho H., Nishiyama Y., Morisaki T.,  
RA Sasaki J., Nakao M., Kuwano A., Nakata M., Ushio Y., Saito H.;  
RT "Cloning and characterization of NE-dlg, a novel human homolog of the  
RT Drosophila discs large (dlg) tumor suppressor protein interacts with  
RL the APC protein.";  
RL Oncogene 14:2425-2433(1997).  
RN [3]  
RP SEQUENCE OF 330-817 FROM N.A.  
RC TISSUE=Brain;  
RX MEDLINE=20039619; PubMed=10574462;  
RA Nogawa T., Ishikawa K.-I., Kikuno R., Hirosewa M., Nomura N.,  
RA Ohara O.;  
RT "Prediction of the coding sequences of unidentified human genes. XV.  
RT The complete sequences of 100 new cDNA clones from brain which code  
RT for large proteins in vitro.";  
RL DNA Res. 6:337-345(1999).  
CC -1- FUNCTION: INTERACTS WITH THE CYTOSOLIC TAIL OF THE NMDA RECEPTOR  
SUBUNIT NR2B (BY SIMILARITY).  
CC -1- SIMILARITY: CONTAINS 3 PDZ/DHR DOMAINS.  
CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.  
CC -1- SIMILARITY: BELONGS TO THE MAGOK FAMILY OF CELL JUNCTION PROTEINS.  
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CC  
CC FMBL: Q49089; AAB61453.1;  
CC EMBL: AB033058; BAA86546.1;  
CC HSSP: Q12959; IPDR.  
CC MIM: 300189;  
CC InterPro: IPR000619; Guanylate\_kin.  
CC InterPro: IPR001478; PDZ.  
CC InterPro: IPR001452; SH3.  
CC Pfam: PF00625; Guanylate\_kin; 1.  
CC Pfam: PF00795; PDZ; 3.  
CC Pfam: PF00018; SH3; 1.  
CC SMART: SM00072; GUKC; 1.  
CC SMART: SM00228; PDZ; 3.  
CC SMART: SM00326; SH3; 1.  
CC PROSITE: PS00856; GUANYLATE\_KINASE\_1; 1.











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DR      EMIL: 014950: AAA9976.1: -.
DR      HSPB: Q12959: 1P0R.
DR      InterPro: IPR000619: Guanylate_kin.
DR      InterPro: IPR001478: PDZ.
DR      InterPro: IPR001452: SH3.
DR      Pfam: PF09625: Guanylate_kin; 1.
DR      Pfam: PF00595: PDZ; 3.
DR      Pfam: PF00018: SH3; 1.
DR      SMART: SM00072: GUKC; 1.
DR      SMART: SM00228: PDZ; 3.
DR      SMART: SM00326: SH3; 1.
DR      PROSITE: PS00856: GUANYLATE_KINASE_1; 1.
DR      PROSITE: PS00852: GUANYLATE_KINASE_2; 1.
DR      PROSITE: PS0106: PDZ; 3.
DR      PROSITE: PS00093: SH3; 1
DR      KW      SH3 domain; Repeat.
KT      DomMain      224      310      P02; 1.
KT      DomMain      418      404      P02; 2.
KT      DomMain      465      545      P02; 3.
KT      DomMain      580      650      SH3.
KT      DomMain      721      911      GUANYLATE_KINASE.
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SC      SOURCE: 911 AA; 100570 MW; 149203100ZAPR06 CDS64;

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Query Match 16.48; Score 192; Hit Length 911;
Post Local Similarity 35.28; Pred. No. 1.5e-06;
Matches 44; Conservative 24; Mismatches 41; Indels 14; Gaps 2;

QY 106 PRVYHFKTHESLGFENWAGKGRKNSPTYSITSPGVAFHFKSLKEDQLLSNVYSVSG 165
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QY 165 EHRKAVETLKAKRSVELVETTFVLEEMAEETK-----IAKRSQV 212
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Db 522 ASRHHKAAALFNRGVAVTIVAGVETRVYSFIVAKLIRVETTRMRGVEVSGSLKESGGR 781

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Db 582 SLVYK 586

RESULT 12
P1=HUMAN
P2=HUMAN
VIEW=ACD; P1=2487 AA;
AC Q129275; Q152564; Q168226; Q152564; Q152655; Q151397;
D1 20-AUG-2001 (Ref. 40); Created)
D1 20-AUG-2001 (Ref. 40); Last sequence updated)

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01 20-DEC-2016 (REV. 4.0). Last amendment update.  
02  
03 19-AUG-2016 (REV. 3.0) AMINO ACIDS, FOR LOCATION 111-136 (REV. 1.1.4.8)  
04 VIOLETIN THIOESTER PHOSPHATASE 1c (VTP1L) (PDB-BAS) (PROTEIN TYROSINE  
05 PHOSPHATASE PTPYL) (FAS-ASSOCIATED PROTEIN-TYROSINE PHOSPHATASE 1)  
06 (FAP-1)).  
07 pPINK3 OR PTPYL OR PTPYL OR PINK1.  
08 Homo sapiens (human).  
09 Enzymatic: EC:2.7.1.1; Cytosolic; Cytoplasmic; Extracellular;  
10 Membrane; Endocytic; Primaries; Carcinoma; Hematopoietic; Bone.  
11 UniProt: Q96067.  
12  
13 SEQUENCE FROM N.A.  
14 TISSUE: Breast carcinoma;  
15 MEDLINE: 94350988; PubMed: 8071359;  
16 Banville D., Ahmad S., Shorro K., Shen S.-H.;  
17 "A novel protein-tyrosine phosphatase with homology to both the  
18 cytoskeletal proteins of the band 4.1 family and junction-associated  
19 transmembrane kinases.";  
20 J. Biol. Chem. 269:22320-22327(1994).  
21  
22 SEQUENCE FROM N.A.; ALTERNATIVE STRUCTURE:  
23 TISSUE: Embryonic;  
24 Medline: 94110679; PubMed: 8297477;  
25 Maekawa K., Imagawa N., Nagamatsu M., Harada S.;  
26 "Molecular cloning of a novel protein tyrosine phosphatase containing  
27 a membrane-binding domain and Glp repeats.";  
28 FEBS Lett. 437:200-206(1994).  
29  
30  
31  
32 SEQUENCE FROM N.A.  
33 TISSUE: Fibroblast;  
34 MEDLINE: 95041119; PubMed: 7929060;  
35 Satas J., Claesson-Welsh L., Heldin C.H., Gomez I.O.;  
36 "Cloning and characterization of PTPN1, a protein tyrosine phosphatase  
37 with similarities to cytoskeletal-associated proteins.";  
38 J. Biol. Chem. 269:24082-24089(1994).  
39  
40  
41  
42 SEQUENCE OF 1216-2490 FROM N.A.  
43 TISSUE: Pancreas;  
44 Wang H.Y.;  
45 J. Biol. Chem. 269:14067-14074(1994).  
46  
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EMBL: U12120; AA060339.1;  
EMBL: U12120; AA04750.1;



PROTEIN: P550106; PDZ: 2.  
CYTOKINE: Chemotaxis.

FT	CHAIN	1	2		INTERFERON-16.
FT	ROBAIN	411	496		PDZ 1.
FT	DOMAIN	533	618		PDZ 2.
FT	CONFLICT	104	104	E > D (IN REF. 2).	
FT	CONFLICT	233	233	F > L (IN REF. 2).	
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5 SVESAPLPAWMLTVVQPLTLR-----IVAAALFLPEGLDSSE-----VYHKKLSLK 54  
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722 SVSSSEMDVAAGSATSALVSPENLESLPETHETITFAFPPVPSVSIGSVI 381  
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55 KVLGSHPGVLPVPGYGMHTTVNCPDEFAPAATKAT----VAAFWASESHHPVV 119  
| | | | |  
982 SLSSSELRLKLDEAVTIIP-----ATLKLDGCHHTLIHKRRG----- 420  
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111 LGTFPELGFNVMGCTE--NSPTYSISFIIPGVAFPGCKRGKGLLVNGVSGVPPGPH 169  
| | | | |  
421 ----ACDLPSLGGSCADLEKRVITVHFPPNPGLASQGETTGCKNNPI.SLNKSTLKSTTH 475  
| | | | |  
170 KAVFLKAARDVKRIIV---PYTPVILPEMAFPFKITA 206  
| | | | |  
476 DALALIDQAEPQAVIVTRKLTPLAMDLSNSTSAASA 515  
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RESULT 15  
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OM25\_HUMAN STANDARD; PRI: 145 AA.

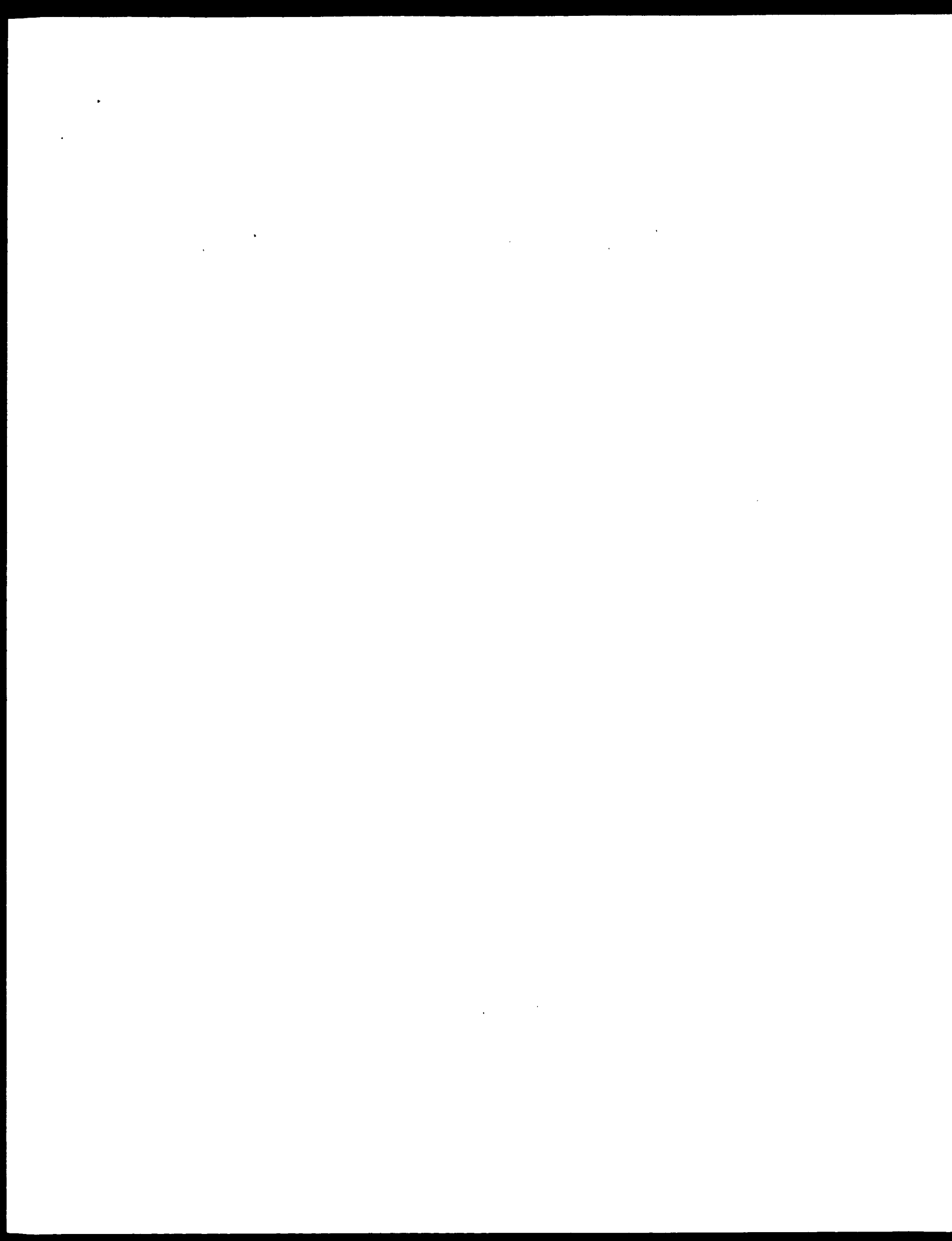
P57105; PDZ: 20 AUG 2001 (Ref. 40, Created)  
P57105; PDZ: 20 AUG 2001 (Ref. 40, Last sequence update)  
P57105; PDZ: 20-AUG-2001 (Ref. 40, Last annotation update)  
MTORC2-SPECIAL OUTER MEMBRANE PROTEIN 25.  
OM25.  
OM25.  
Homo sapiens (Human).  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eularchia; Primates; Catarrhini; Hominoidea; Homo.  
NCBI TaxId:9606;  
NM\_111  
SEQUENCE FROM N.A.  
RC TISSUE:Placenta;  
VA Itoyai T., Oda T., Hayashi K., Saitama T., Hosoi T., Suzuki Y.,  
Nishiyama W., Nagai K., Sugano S., Shiratori A., Sudo H.,  
Watanabe M., Hosoki J., Kaki Y., Kodaira H., Kondo H., Sugawara M.,  
Watanabe K., Ohba Y., Ishida S., Morikawa K., Imai Y., Takiguchi S.,  
Yamamoto T., Wakatsuki A., Nakamura Y., Nawahori K., Masuko Y.,  
Nikitina K., Izajima T.;  
Submitted (Feb-2003) to the EMBL/GenBank/DDBJ databases.  
-1- SUBMITTER LOCATION: MITOCHONDRIAL OUTER MEMBRANE (BY  
SIMILIARITY)

-1- SIMILIARITY CONTAINS 1 PDZ/DHR DOMAIN

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EMBL AK032133; BAM92398.1; -  
InterPro: IPRO0478, PDZ.  
DR Pfam: PF05755, PDZ\_1













1 APPLICANT: As Young, Janice  
 2 APPLICANT: Patterson, Claudia  
 3 TITLE OF INVENTION: CELL INJECTION FOR FERTILIZATION  
 4 FILE REFERENCE: 87-0599 US  
 5 CURRENT APT. PAT. # NUMBER: 05/06,330, 192  
 6 CURRENT FILING DATE: 1999-08-06  
 7 EARLIER APT. PAT. # NUMBER: 09/151,611  
 8 EARLIER FILING DATE: 1998-09-11  
 9 NUMBER OF SEQ. ID NOS.: 3  
 10 SOFTWARE: PERL program  
 11 SEQ. ID NO. 1  
 12 LENGTH: 234  
 13 TYPE: PRT  
 14 ORGANISM: Homo sapiens  
 15 FEATURE:  
 16 OTHER INFORMATION: 1974-837  
 17 US-09-370-102-1

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Best Local Similarity:	100.0%	Pred. No. 1,40-169		
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			Gaps	0

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D0	1	MKPSVTSATATAMKAVIIVOPITEDIPVAALTELKIJOSDZVPRKIOSIKVIGOSE	60
QY	1	MKPSVTSATATAMKAVIIVOPITEDIPVAALTELKIJOSDZVPRKIOSIKVIGOSE	60
D0	1	MKPSVTSATATAMKAVIIVOPITEDIPVAALTELKIJOSDZVPRKIOSIKVIGOSE	60
QY	61	FCTAIPRVCVMMPITTVNOSTEPBPAPAAIAVAVANASGDSHPVVCLPTEGCSLGF	120
D0	61	FCTAIRVCVCMMPITTVNOSTEPBPAPAAIAVAVANASGDSHPVVCLPTEGCSLGF	120
QY	121	NWMDKRDNSPTTSTIPGGVAEBHSGIKRDLGLSYNVSVGRPHNEKAVELLSAAD	180
D0	121	NWMDKRLNSPTTSTIPGGVAEBHSGIKRDLGLSYNVSVGRPHNEKAVELLSAAD	180
QY	181	SVKLVVPIPKVLFEDEARFELTPARPPOCGGTTTTGGGGGGGGGGGGGGGGGG	233
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1 RESULT
2 US-09-151-611-3
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4 : Sequence 3, Application US/09151611
5 : Patent No. 5958741
6 :
7 : GENERAL INFORMATION
8 :
9 : APPLICANT: Yuc, Henry
10 :
11 : APPLICANT: Au-Young, Janice
12 :
13 : APPLICANT: Patterson, Jonda
14 :
15 : TITLE OF INVENTION: CELL JUNCTION PDZ PROTEIN
16 :
17 : FILE REFERENCE: 09-0559 US
18 :
19 : CURRENT APPLICATION NUMBER: US/09/151-611
20 :
21 : CURRENT FILING DATE: 1998-03-11
22 :
23 : NUMBER OF SEQ. ID NOS: 3
24 :
25 : SOFTWARE: PEPL Program
26 :
27 : SEQ ID NO: 3
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29 : LENGTH: 247
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31 : TYPE: PRT
32 :
33 : ORGANISM: Caenorhabditis elegans
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35 : FEATURE: -
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37 : OTHER INFORMATION: 41685067
38 :
39 : US-09-151-611-3

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Query Match: 55.0%; Score: 64.5; IP: 2; Length: 237;  
 Best Local Similarity: 70.6%; Pred. No. 1: 56;  
 Matches: 127; Conservative: 23; Indels: 1; Gaps: 1

[illegible][illegible]

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1 RESULT 4
2 US-09-470-102-4
3 Sequence 4: Application US/09370102
4 Patent No. 6265547
5 GENERAL INFORMATION:
6 APPLICANT: Yue, Henry
7 APPLICANT: Au-Yang, Janice
8 APPLICANT: Patterson, Chandra
9 TITLE OF INVENTION: CELL JUNCTION PROTEIN
10 FILE REFERENCE: PE-0599 US
11 CURRENT APPLICATION NUMBER: 09/470,102
12 CURRENT FILING DATE: 1999-08-06
13 EARLIER APPLICATION NUMBER: 09/151,611
14 EARLIER FILING DATE: 1998-09-11
15 REFERENCE: Also in NOS: 3
16 SOFTWARE: Perl program
17 SEQ ID NO 3
18 LENGTH: 297
19 TYPE: PRM
20 ORGANISM: Caenorhabditis elegans
21 FEATURES: -
22 OTHER INFORMATION: q1685067
23 US-09-470-102-4

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Query Match	55.08	Score 643.5	PI 4	Length 297
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[illegible]

RESULT 5  
 05-08-596-291-4  
 Sequence 3, Application 03/08596291  
 Patent No. 5821075  
 CEREAL INFORMATION:  
 APPLICANT: GOMEZ, LEONEL JORGE  
 APPLICANT: SARAS, JAN  
 APPLICANT: CLARSSON, WELSH, LENA  
 APPLICANT: HELDIN, CARL-HENRIK  
 TITLE OF INVENTION: PRIMARY STRUCTURE AND FUNCTIONAL  
 TITLE OF INVENTION: EXPRESSION OF NUCLEOTIDE SEQUENCES FOR N-VEL PROTEIN  
 NUMBER OF SEQUENCES: 4  
 CORRESPONDENCE ADDRESS:  
 APPLICANT: WOLFF, GREENFIELD & SARAS, P.C.  
 STREET: 600 ATLANTIC AVENUE  
 CITY: BOSTON  
 STATE: MASSACHUSETTS  
 COUNTRY: USA  
 ZIP: 02210  
 C. FURTHER RETAINABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMMENTS: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS

APPLICAIION NUMBER: US/09/100,804

US-09-080-855-12

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1 RESULT 5
2 US-09-100-804-3
3 Sequence 3, Application 05/09100804
4 Patent No. 6066472
5
6 GENERAL INFORMATION:
7
8 APPLICANT: GOMEZ, LEONEL JORGE
9
10 APPLICANT: SARAS, JAN
11
12 APPLICANT: CLAESSON-WEISS, LENA
13
14 APPLICANT: HELDIN, CARL-HEINRICH
15
16 TITLE OF INVENTION: PRIMARY STRUCTURE AND FUNCTIONAL
17
18 TITLE OF INVENTION: EXPRESSION OF NOVELTIDIO SEQUENCES FOR N-LEVEL PROTEIN
19
20 NUMBER OF SEQUENCES: 34
21
22 CORRESPONDENCE ADDRESS:
23
24 ADDRESSEE: WATTE, CHRISTOPH & SACKS, P.L.L.
25
26 STREET: 600 ATLANTIC AVENUE
27
28 CITY: BOSTON
29
30 STATE: MASSACHUSETTS
31
32 COUNTRY: USA
33
34 ZIP: 02210
35
36 COMPUTER READABLE FORM:
37
38 MEDIUM TYPE: Floppy disk
39
40 COMPUTER: IBM PC compatible
41
42 OPERATING SYSTEM: PC DOS/MS-DOS
43
44 SOFTWARE: PatentIn Release #1.0, Version #1.25
45
46 CURRENT APPLICATION DATA:
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48 APPLICATION NUMBER: US/09/100,804

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[illegible]

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1      RESULT      8
2      PCT-US94-09943-2
3      Sequence 2, Application EC/7089409943
4      GENERAL INFORMATION:
5      APPLICANT:
6      APPLICANT:
7      APPLICANT:
8      APPLICANT:
9      APPLICANT:
10     TITLE OF INVENTION: PRIMARY STRUCTURE AND FUNCTIONAL
11     TITLE OF INVENTION: EXPRESSION OF NOVELTY SEQUENCES FOR NOVEL PROTEIN
12     TITLE OF INVENTION: TYROSINE PHOSPHATASES
13     NUMBER OF SEQUENCES: 4
14     CORRESPONDENCE ADDRESS:
15     STREET: 600 ATLANTIC AVENUE
16     CITY: BOSTON
17     STATE: MASSACHUSETTS
18     COUNTRY: USA
19     COMPUTER READABLE FORM:
20     MEDIUM TYPE: 5.25" disk
21     COMPUTER: IBM PC compatible
22     OPERATING SYSTEM: PC DOS MS-DOS
23     SOFTWARE: Patent In Release #1.0, Version #1.25
24     CURRENT APPLICATION DATA:
25     APPLICATION NUMBER: PCT/US94/09943
26     FILING DATE: 01-SEP-1994
27     CLASSIFICATION:
28     PRIOR APPLICATION DATA:
29     APPLICATION NUMBER: US 08/115,573
30     FILING DATE: 01-SEP-1993
31     ATTORNEY/AGENT INFORMATION:
32     NAME: TWOMEY, MICHAEL, J.
33     REGISTRATION NUMBER: P-48,790
34     REFERENCE/EXCIT NUMBER: 1-461,700 (W)
35     TELECOMMUNICATION INFORMATION:
36     TELEPHONE: 617/720-3500
37     TELEFAX: 617/720-2411
38     TELEX: 92-1742 EREXEL
39     INFORMATION FOR SEQ ID NO: 2:
40     SEQUENCE CHARACTERISTICS:
41     LENGTH: 2466 amino acids
42     TYPE: amino acid
43     TOPOLOGY: linear
44     MOLECULE TYPE: protein
45     PCT-US94-09943-2

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Query Match	15.48;	Score 180.5;	DB 5;	Length 2466;
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[illegible]

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1  RESULT          9
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3  : Sequence 3, Application US/09106998
4  : Patent No. 6,291,173
5  :
6  : GENERAL INFORMATION:
7  :
8  : APPLICANT: Bartels, Paul L.
9  :
10 : APPLICANT: Davididan, Sean V.
11 :
12 : TITLE OF INVENTION: MMS2: An MMS1 Interacting Protein
13 :
14 : FILE REFERENCE: MMS2
15 :
16 : CURRENT APPLICATION NUMBER: US/09/306,998
17 :
18 : EARLIER FILING DATE: 1999-05-07
19 :
20 : EARLIER APPLICATION NUMBER: US 6,070,84,740
21 :
22 : NUMBER OF SEQ. ID NOS.: 72
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24 : SOFTWARE: Patent In Ver. 2.0
25 :
26 : SEQ. ID NO. 3
27 :
28 : LENGTH: 2017
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30 : TYPE: PRT
31 :
32 : ORGANISM: Homo sapiens
33 :
34 : US-09-106-998-4

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	14,982	Score 174.51	DB 4:	Length 2837
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RESULT 10  
 US-09-100-804-16  
 Sequence 16, Application 02/09100804  
 Patent No. 6564722  
 GENERAL INFORMATION:  
 APPLICANT: CARRE, HERNED JORGE  
 APPLICANT: SARAS, JAN  
 APPLICANT: CLAESON-WELSH, LENA  
 APPLICANT: HELDIN, CARL-HENRIK  
 TITLE OF INVENTION: PRIMARY STRUCTURE AND FUNCTIONAL  
 TITLE OF INVENTION: EXPRESSION OF NUCLEOTIDE SEQUENCES FOR N-VIL PROTEIN  
 TITLE OF INVENTION: TYROSINE PHOSPHATASES  
 NUMBER OF SEQUENCES: 34  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: WOLF, GREENFIELD & SACKS, P.C.  
 STREET: 600 ATLANTIC AVENUE  
 CITY: BOSTON  
 STATE: MASSACHUSETTS  
 COUNTRY: USA  
 ZIP: 02210  
 COMPUTER READABLE FORM:

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1 CURRENT APPLICATION DATA:
2 APPLICATION NUMBER: 05/08/545,860
3 FILING DATE: 07-MAR-1996
4 CLASSIFICATION: 435
5 PRIOR APPLICATION DATA:
6 ACT. NO.: 5,206,616 04/96
7 FILING DATE: 22-APR-1994
8 PRIOR APPLICATION DATA:
9 APPLICATION NUMBER: 08/10/592,109/40
10 FILING DATE: 05-DEC-1992
11 PRIOR APPLICATION DATA:
12 APPLICATION NUMBER: 05/08/427,392
13 FILING DATE: 19-0CT-1994
14 PRIOR APPLICATION DATA:
15 ACT. NO.: 5,206,616 04/96
16 FILING DATE: 11-0CT-1994
17 PRIOR APPLICATION DATA:
18 APPLICATION NUMBER: 05/08/062,444
19 FILING DATE: 14-MAY-1994
20 PRIOR APPLICATION DATA:
21 APPLICATION NUMBER: 05/07/671,094
22 FILING DATE: 30-0CT-1992
23 PRIOR APPLICATION DATA:
24 APPLICATION NUMBER: 05/07/988,839
25 FILING DATE: 27-MAY-1992
26 PRIOR APPLICATION DATA:
27 APPLICATION NUMBER: 05/07/805,094
28 FILING DATE: 11-DEC-1991
29 ATTORNEY/AGENT INFORMATION:
30 NAME: DeLuca Esq., Mark
31 REGISTRATION NUMBER: 43,429
32 REFERENCE/MARKET NUMBER: 179-1262
33 TELECOMMUNICATION INFORMATION:
34 TELEPHONE: (215) 568-4100
35 TELEFAX: (215) 568-4449
36 INFORMATION PER SEQ. ID NO.: 54:
37 SOURCE CHARACTERISTICS:
38 LENGTH: 60 amino acids
39 TYPE: amino acid
40 STRANDEDNESS: single
41 TOPOLOGY: linear
42 MOLECULE TYPE: protein
43 HYDROPHILIC: NO
44 ANTI-SENSE: NO
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46 05-08-545-8600-54
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STREET: One Liberty Place, 46th floor  
CITY: Philadelphia  
STATE: Pennsylvania  
COUNTRY: USA  
ZIP: 19103  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/04496  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: DeLuca Esq., Mark  
REGISTRATION NUMBER: 43,229  
REFERENCE/EXCERPT NUMBER: 100-1242  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (215) 568-4100  
TELEFAX: (215) 568-4449  
INFORMATION FOR SEQ ID NO: 54:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 80 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYDROPHILIC: NO  
ANTI-SENSE: NO  
PCT-US94-04496-54

Query Match 14.4% Score 170.5 DB 5 Length 80  
Best Local Similarity 46.8% Pred. No. 4, 1e-10  
Matches 37: Conservative 14: Mismatches 27: Indels 1: Gaps 1:

QY 113 KTHPELEFNNWQKPNSPVTSPTPCVAFPHCH FQSGVLLSVYSECEHIERAV 172  
DB 1 PTHPELEFNNWQKPNSPVTSPTPCVAFPHCH FQSGVLLSVYSECEHIERAV 59

QY 173 ELKAAEYSVEIVVETK 191  
DB 60 GAKKISGVVLLAQVPE 78

RESULT 13  
US-09-290-640-46  
Sequence 46, Application US/09290640  
Patent No. 6204055  
GENERAL INFORMATION:  
APPLICANT: Ivan, Nicholas M.  
APPLICANT: Matroussou, Effie G.  
TITLE OF INVENTION: Antisense compound Modulation of Fas Mediated Signaling  
FILE REFERENCE: ISPH-0451  
CURRENT FILING DATE: 1999-04-12  
NUMBER OF SEQ ID NOS: 85  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 46  
LENGTH: 2485  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-290-640-46

Query Match 14.4% Score 169 DB 4 Length 2485  
Best Local Similarity 28.4% Pred. No. 7, 9e-08  
Matches 40: Conservative 26: Mismatches 14: Indels 32: Gaps 2:

QY 78 VNRTRKATKATKATVAANAASHSHR-----V 108  
DB 1409 ISTRVYSTRVSTMTAFATSSSGPFLKSSSSVNISSMNFLESSSPKADUHE 1308

QY 109 VETPTPEPCFNNWQKPNSPVTSPTPCVAFPHCH FQSGVLLSVYSECEHIERAV 165  
DB 1309 VETPTPEPCFNNWQKPNSPVTSPTPCVAFPHCH FQSGVLLSVYSECEHIERAV 1428

QY 106 FRRGAVELKAAEYSVEIVVETK 186  
DB 1429 ATRQAVETLKRNGQVYHLL 1449

RESULT 14  
US-09-100-804-28  
Sequence 28, Application US/09100804  
Patent No. 6066472  
GENERAL INFORMATION:  
APPLICANT: CONZ, LIONEL JORGE  
APPLICANT: SARAS, JAN  
APPLICANT: CLAESSEN WILSH, LENA  
APPLICANT: HELDIN, CARL-HENRIK  
TITLE OF INVENTION: PRIMARY STRUCTURE AND FUNCTIONAL  
TITLE OF INVENTION: EXPRESSION OF RECOMBINANT SEQUENCES FOR NEW PROTEIN  
TITLE OF INVENTION: TYROSINE PHOSPHATASES  
NUMBER OF SEQUENCES: 34  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: WOLF, GREENFIELD & SACKS, P.C.  
STREET: 600 ATLANTIC AVENUE  
CITY: BOSTON  
STATE: MASSACHUSETTS  
COUNTRY: USA  
ZIP: 02210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/100,404  
FILING DATE:  
CLASSIFICATION:  
FASL APPLICATION DATA:  
APPLICATION NUMBER: US-08/596,291  
FILING DATE: 09-AUG-1996  
APPLICATION NUMBER: US-08/215,573  
FILING DATE: 01-SEP-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/09943  
FILING DATE: 01-SEP-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: GATES, EDWARD R.  
REGISTRATION NUMBER: 31,616  
REFERENCE/EXCERPT NUMBER: 1-451,7004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-720-4500  
TELEFAX: 617-720-2441  
INDEX:  
IM PRACTICE NO. 28:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 73 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYDROPHILIC: NO  
ANTI-SENSE: NO  
US-09-100-804-28

Query Match 13.4% Score 166.5 DB 3 Length 73  
Best Local Similarity 47.8% Pred. No. 9, 1e-09  
Matches 33: Conservative 13: Mismatches 22: Indels 1: Gaps 1:

QY 117 ATRQAVETLKRNGQVYHLL 1449  
DB 1429 ATRQAVETLKRNGQVYHLL 1449

db 5 GLOPNVWG-EDGEGTIFSLIAGPADLSPIKRODILSVNGVDLKNASHEQATALK 63

UY 177 AAKDSYKLV 185

db 64 NAGQIVTII 72

## RESULT 15

US-08-410-804-1

? Sequence 1, Application US/08410804

? Patent No. 5612994

? GENERAL INFORMATION:

? APPLICANT: Reed, John C.

? APPLICANT: Sato, Takaaki

? TITLE OF INVENTION: FAS ASSOCIATED PROTEINS

? NUMBER OF SEQUENCES: 22

? CORRESPONDENCE ADDRESS:

? ADDRESSEE: Cathryn Campbell

? STREET: 4370 La Jolla Village Drive, Ste 700

? CITY: San Diego

? STATE: California

? COUNTRY: United States

? ZIP: 92122

? COMPUTER READABLE FORM:

? MEDIUM TYPE: Floppy disk

? COMPUTER: IBM PC compatible

? OPERATING SYSTEM: PC-DOS/MS-DOS

? SOFTWARE: Patent in release #1.0, Version #1.25

? CURRENT APPLICATION DATA:

? APPLICATION NUMBER: US/08/410,804

? FILING DATE: 27-MAR-1995

? CLASSIFICATION: 435

? PRIOR APPLICATION DATA:

? APPLICATION NUMBER: US 08/259,514

? FILING DATE: 14-JUN-1994

? ATTORNEY/AGENT INFORMATION:

? NAME: Campbell, Cathryn

? REGISTRATION NUMBER: 31,815

? REFERENCE/TICKET NUMBER: P-LJ 1389

? TELECOMMUNICATION INFORMATION:

? TELEPHONE: (619) 535-9001

? TELEFAX: (619) 535-8949

? INFORMATION FOR SEQ ID NO: 1:

? SEQUENCE CHARACTERISTICS:

? LENGTH: 610 amino acids

? TYPE: amino acid

? TOPOLOGY: linear

? MOLECULE TYPE: protein

US-08-410-804-1

Query Match 13.4%; Score 156.5; Dh 1; Length 610;

Best Local Similarity 27.4%; Pred. No. 1.9e-07;

Matches 40; Conservative 26; Mismatches 43; Indels 37; Gaps 3;

UY 78 VNCQPEPKARATAKATVAFAFASGSHPR-----V 108

db 31 ISQVTVSPKPSQMEGATVYSSQWQTPKQTSVSVTPRPNRKTSPPPGDIE 90

UY 109 VHLPTKTRGQFNV-----MGR---KQNSPIYISPIPGVATPHGDKRGQLISNG 160

db 91 VPLAKPNSTGISTVI EDPKQVNSVSNQIYVAVIFGCAAEEDPTIKQDVLAVNG 150

UY 161 VSEGEHEKAEVLKAADSVKLV 186

db 151 VSEEGATHKQAVETLRNTQGVVHLL 176

Search completed: May 7, 2002, 12:41:41  
Job time: 111 sec

